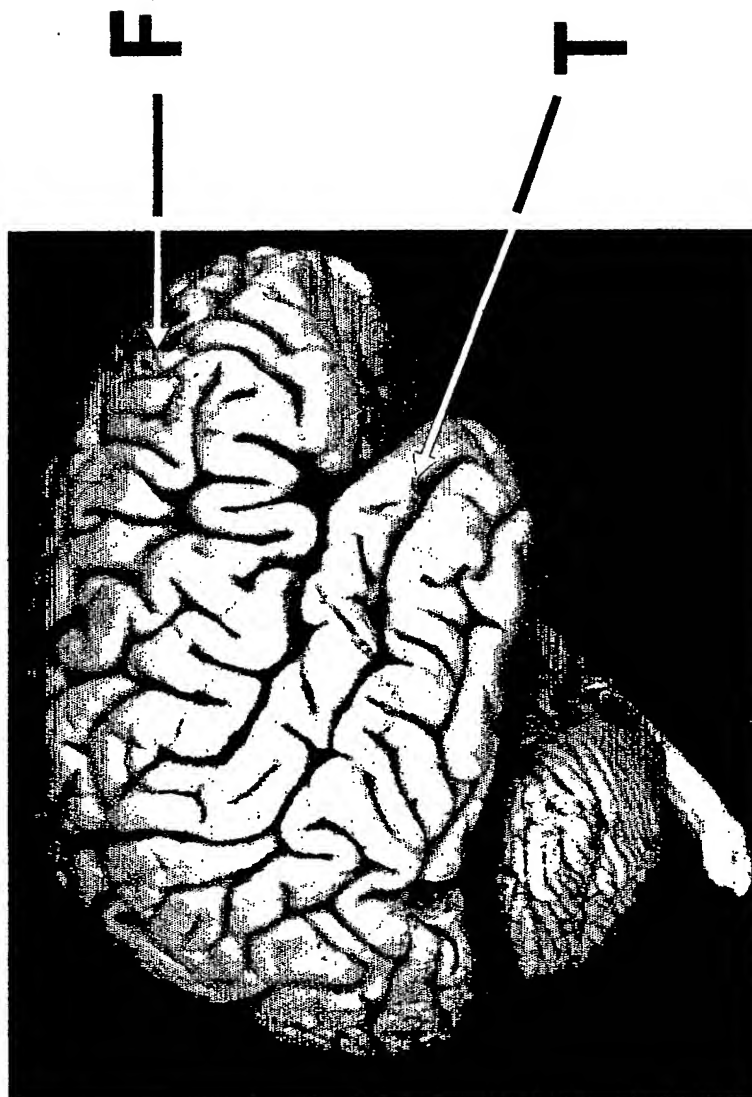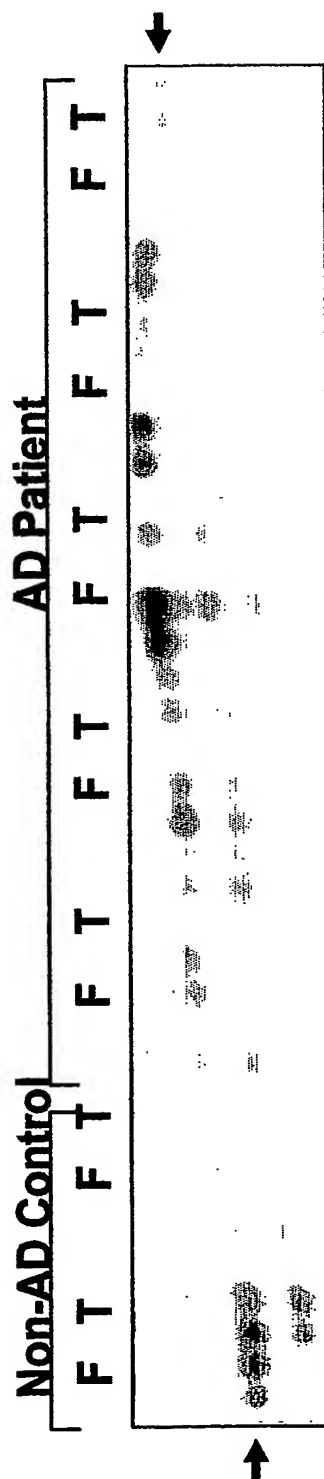Fig. 1: Identification of Genes Involved in Alzheimer's Disease Pathology

Fig. 2:Identification of differentially expressed genes
in a fluorescence differentialdisplay screen

Figure 3: SEQ ID NO. 1

Length: 36 bp

1 AGTTAAGTTT CTTTGTAAAA CACTGATTTT TTCTCC

-4/25-

Fig. 4: Alignment of SEQ ID NO. 1 with human golgin-245 cDNA (GenBank accession number U41740)

```
  36 GGAGAAAAAATCAGTGTTTTACAAAGAAACTTAACT 1
     | |||||||||||||||||||||||||||||||||||
5488 GAAGAAAAAATCAGTGTTTTACAAAGAAACTTAACT 5523
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-5/25-

Fig. 5: SEQ ID NO. 2: amino acid sequence of human golgin-245, splice variant 1

Length: 2228 aa

```
   1  MFKKLKQKIS  EEQQQLQQAL  APAQASSNSS  TPTRMRSRTS  SFTEQLDEGT
  51  PNRESGDTQS  FAQKLQLRVP  SVESLFRSPI  KESLFRSSSK  ESLVRTSSRE
 101  SLNRLDLDSS  TASFDPPSDM  DSEAEDLVGN  SDSLNKEQLI  QRLRRMERSL
 151  SSYRGKYSEL  VTAYQMLQRE  KKKLQGILSQ  SQDKSLRRIA  ELREELQMDQ
 201  QAKKHLQEEF  DASLEEKDQY  ISVLQTQVSL  LKQRLRNGPM  NVDVLKPLPQ
 251  LEPQAEVFTK  EENPESDGEP  VVEDGTSVKT  LETLQQRVKR  QENLLKRCKE
 301  TIQSHKEQCT  LLTSEKEALQ  EQLDERLQEL  EKIKDLHMAE  KTKLITQLRD
 351  AKNLIEQLEQ  DKGMVIAETK  RQMHETLEMK  EEEIAQLRSR  IKQMTTQGEE
 401  LREQKEKSER  AAFEELEKAL  STAQKTEEAR  RKLKAEMDEQ  IKTIEKTSEE
 451  ERISLQQELS  RVKQEVVDVM  KKSSEEQIAK  LQKLHEKELA  RKEQELTKKL
 501  QTREREFQEQ  MKVALEKSQS  EYLKISQEKE  QQESLALEEL  ELQKKAILTE
 551  SENKLRDLQQ  EAETYRTRIL  ELESSLEKSL  QENKNQSKDL  AVHLEAEKNK
 601  HNKEITVMVE  KHKTELESLK  HQQDALWTEK  LQVLKQQYQT  EMEKLREKCE
 651  QEKETLLKDK  EIIFQAHIEE  MNEKTLEKLD  VKQTELESLS  SELSEVLKAR
 701  HKLEEELSVL  KDQTDKMKQE  LEAKMDEQKN  HHQQQVDSII  KEHEVSIQRT
 751  EKALKDQINQ  LELLLKERDK  HLKEHQAHVE  NLEADIKRSE  GELQQASAKL
 801  DVFQSYQSAT  HEQTKAYEEQ  LAQLQQKLLD  LETERILLTK  QVAEVEAQKK
 851  DVCTELDAHK  IQVQDLMQQL  EKQNSEMEQK  VKSLTQVYES  KLEDGNKEQE
 901  QTKQILVEKE  NMILQMREGQ  KKEIEILTQK  LSAKEDSIHI  LNEEYETKFK
 951  NQEKKMEKVK  QKAKEMQETL  KKKLLDQEAK  LKKELENTAL  ELSQKEKQFN
1001  AKMLEMAQAN  SAGISDAVSR  LETNQKEQIE  SLTEVHRREL  NDVISIWEKK
1051  LNQQAEELQE  IHEIQLQEKE  QEVAELKQKI  LLFGCEKEEM  NKEITWLKEE
1101  GVKQDTTLNE  LQEQLKQKSA  HVNSLAQDET  KLKAHLEKLE  VDLNKSLKEN
1151  TFLQEQLVEL  KMLAEEDKRK  VSELTSKLKT  TDEEFQSLKS  SHEKSNKSLE
1201  DKSLEFKKLS  EELAIQLDIC  CKKTEALLEA  KTNELINISS  SKTNAILSRI
1251  SHCQHRTTKV  KEALLIKTCT  VSELEAQLRQ  LTEEQNTLNI  SFQQATHQLE
1301  EKENQIKSMK  ADIESLVTEK  EALQKEGGNQ  QQAASEKESC  ITQLKKELSE
1351  NINAVTLMKE  ELKEKKVEIS  SLSKQLTDLN  VQLQNSISLS  EKEAAISSLR
1401  KQYDEEKCEL  LDQVQDLSFK  VDTLSKEKIS  ALEQVDDWSN  KFSEWKKKAQ
1451  SRFTQHQNTV  KELQIQLELK  SKEAYEKDEQ  INLLKEELDQ  QNKRFDCLKG
1501  EMEDDKSKME  KKESNLETEL  KSQTARIMEL  EDHITQKTIE  IESLNEVLKN
1551  YNQQKDIEHK  ELVQKLQHFQ  ELGEEKDNRV  KEAEEKILTL  ENQVYSMKAE
1601  LETKKKELEH  VNLSVKSKEE  ELKALEDRLE  SESAAKLAEL  KRKAEQKIAA
1651  IKKQLLSQME  EKEEQYKKGT  ESHLSELNTK  LQEREREVHI  LEEKLKSVES
1701  SQSETLIVPR  SAKNVAAYTE  QEEADSQGCV  QKTYEEKISV  LQRNLTEKEK
1751  LLQRVGQEKE  ETVSSHFEMR  CQYQERLIKL  EHAEAKQHED  QSMIGHLQEE
1801  LEEKNKKYSL  IVAQHVEKEG  GKNNIQAKQN  LENVFDDVQK  TLQEKELTCQ
1851  ILEQKIKELD  SCLVRQKEVH  RVEMEELTSK  YEKLQALQQM  DGRNKPTELL
1901  EENTEEKSKS  HLVQPKLLSN  MEAQHNDLEF  KLAGAEREKQ  KLGKEIVRLQ
1951  KDLRMLRKEH  QQELEILKKE  YDQEREEKIK  QEQEDLELKH  NSTLKQLMRE
2001  FNTQLAQKEQ  ELEMTIKETI  NKAQEVEAEL  LESHQEETNQ  LLKKIAEKDD
2051  DLKRTAKRYE  EILDAREEEM  TAKVRDLQTQ  LEELQKKYQQ  KLEQEENPGN
2101  DNVTIMELQT  QLAQKTTLIS  DSKLKEQEFR  EQIHNLEDRL  KKYEKNVYAT
2151  TVGTPYKGGN  LYHTDVSLFG  EPTEFEYLRK  VLFEYMMGRE  TKTMAKVITT
2201  VLKFPDDQTQ  KILEREDARL  MSWLRSSS
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Fig. 6: SEQ ID NO. 3: nucleotide sequence of human golgin-245 cDNA,   splice variant 1

Length: 7636 bp

```
   1   GCAACGAAGG TACCATGGCC GTTGTCGTCG CCGCCGCGGC TCCCGGGGCT
  51   GGATGGGGGG CCGAGGCCAG CCAGTGGCAC CCGGAAGAAA GAGACGCGGC
 101   GGCGGCGACG CCGACACCCT CAGGACGAGT GTCCGGACTT GCCCACAGCC
 151   TCAAGGAGGA GACGGCGAGG CCCGGCCCCC GCTGTCCCTG GTGTAAAGAA
 201   GTCGCCGTAG CCGTCGCGGC CGGGACTCCC CGGGCTCTCG CCCTTCAGGT
 251   TTCGTTGACA CTCAGGACCG TACGTACGCT GCGCCATGTT CAAGAAACTG
 301   AAGCAAAAGA TCAGCGAGGA GCAGCAGCAG CTCCAGCAGG CGCTGGCTCC
 351   TGCTCAGGCG TCCTCCAATT CTTCAACACC AACAAGAATG AGGAGCAGGA
 401   CATCTTCATT TACAGAGCAA CTTGATGAAG GTACACCCAA TAGAGAGTCA
 451   GGTGACACAC AGTCTTTTGC ACAGAAGCTC CAGCTCCGGG TGCCCTCCGT
 501   GGAGTCTTTG TTTCGAAGTC CGATAAAGGA ATCTCTATTC CGGTCTTCTT
 551   CTAAAGAGTC TTTGGTACGA ACATCTTCCA GAGAATCCCT GAATCGACTT
 601   GACCTGGACA GTTCTACTGC CAGTTTTGAT CCACCCTCTG ATATGGATAG
 651   CGAGGCTGAA GACTTGGTAG GGAATTCAGA CAGTCTCAAC AAAGAACAGT
 701   TGATTCAGCG GTTGCGAAGA ATGGAACGAA GCTTAAGTAG CTACAGGGGA
 751   AAATATTCTG AGCTTGTTAC AGCTTATCAG ATGCTTCAGA GAGAGAAGAA
 801   AAAGCTACAA GGTATATTAA GTCAGAGTCA GGATAAATCA CTTCGGAGAA
 851   TAGCAGAATT AAGAGAGGAG CTCCAAATGG ACCAGCAGGC AAAGAAACAT
 901   CTGCAAGAGG AGTTTGATGC ATCTTTAGAG GAGAAAGATC AGTATATCAG
 951   TGTTCTCCAA ACTCAGGTTT CTCTACTGAA ACAACGATTA CGAAATGGCC
1001   CGATGAATGT TGATGTACTG AAACCACTTC CTCAGCTGGA ACCACAGGCT
1051   GAAGTCTTCA CTAAAGAAGA GAATCCAGAA AGTGATGGAG AGCCAGTAGT
1101   GGAAGATGGA ACTTCTGTAA AAACACTGGA AACACTCCAG CAAAGAGTGA
1151   AGCGTCAAGA GAACCTACTT AAGCGTTGTA AGGAAACAAT TCAGTCACAT
1201   AAGGAACAAT GTACACTATT AACTAGTGAA AAAGAAGCTC TGCAAGAACA
1251   ACTGGATGAA AGACTTCAAG AACTAGAAAA GATAAAGGAC CTTCATATGG
1301   CCGAGAAGAC TAAACTTATC ACTCAGTTGC GTGATGCAAA GAACTTAATT
1351   GAACAGCTTG AACAAGATAA GGGAATGGTA ATCGCAGAGA CAAAACGTCA
1401   GATGCATGAA ACCCTGGAAA TGAAAGAAGA AGAAATTGCT CAACTCCGTA
1451   GTCGCATCAA ACAGATGACT ACCCAGGGAG AGGAATTACG GGAACAGAAA
1501   GAAAAGTCCG AAAGAGCTGC TTTTGAGGAA CTTGAAAAAG CTTTGAGTAC
1551   AGCCCAAAAA ACAGAGGAAG CACGGAGAAA ACTGAAGGCA GAAATGGATG
1601   AACAAATAAA AACTATCGAA AAAACAAGTG AGGAGGAACG CATCAGTCTT
1651   CAACAGGAAT TAAGTCGGGT GAAACAGGAG GTTGTTGATG TAATGAAAAA
1701   ATCCTCAGAA GAACAAATTG CTAAGCTACA GAAGCTTCAT GAAAAGGAGC
1751   TGGCCAGAAA AGAGCAGGAA CTGACCAAGA AGCTTCAGAC CCGAGAAAGG
1801   GAATTTCAGG AACAAATGAA AGTAGCTCTT GAAAAGAGTC AATCAGAATA
1851   TTTGAAGATC AGCCAAGAAA AGAACAGCA AGAATCTTTG GCCCTAGAAG
1901   AGTTAGAGTT GCAGAAAAAA GCAATCCTCA CAGAAAGTGA AAATAAACTT
1951   CGGGACCTTC AGCAAGAAGC AGAGACTTAC AGAACTAGAA TTCTTGAATT
2001   GGAAAGTTCT TTGGAAAAAA GCTTACAAGA AAACAAAAAT CAGTCAAAAG
2051   ATTTGGCTGT TCATCTGGAA GCTGAAAAAA ATAAGCACAA TAAGGAGATT
2101   ACAGTCATGG TTGAAAAACA CAAGACAGAA TTGGAAAGCC TTAAGCATCA
2151   GCAGGATGCC CTTTGGACTG AAAAACTCCA AGTCTTAAAG CAACAATATC
2201   AGACTGAAAT GGAAAAACTT AGGGAAAAGT GTGAACAAGA AAAAGAAACA
2251   TTGTTGAAAG ACAAAGAGAT TATCTTCCAG GCCCACATAG AAGAAATGAA
2301   TGAAAAGACT TTAGAAAAGC TTGATGTGAA GCAAACAGAA CTAGAATCAT
2351   TATCTTCTGA ACTGTCAGAA GTATTAAAAG CCCGTCACAA ACTAGAAGAG
2401   GAACTTTCTG TTCTGAAAGA TCAAACAGAT AAAATGAAGC AGGAATTAGA
2451   GGCCAAGATG GATGAACAGA AAAATCATCA CCAGCAGCAA GTTGACAGTA
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2501  TCATTAAAGA  ACACGAGGTA  TCTATCCAGA  GGACTGAGAA  GGCATTAAAA
2551  GATCAAATTA  ATCAACTTGA  GCTTCTCTTG  AAGGAAAGGG  ACAAGCATTT
2601  GAAAGAGCAT  CAGGCTCATG  TAGAAAATTT  AGAGGCAGAT  ATTAAAAGGT
2651  CTGAAGGGGA  ACTCCAGCAG  GCATCTGCTA  AGCTGGACGT  TTTTCAGTCT
2701  TACCAGAGTG  CCACACATGA  GCAGACAAAA  GCATATGAGG  AACAGTTGGC
2751  CCAATTGCAG  CAGAAGTTGT  TGGATTTGGA  AACAGAAAGA  ATTCTTCTTA
2801  CCAAACAGGT  TGCTGAAGTT  GAAGCACAAA  AGAAAGATGT  TTGTACTGAG
2851  TTAGATGCTC  ACAAAATCCA  GGTGCAGGAC  TTAATGCAGC  AACTTGAAAA
2901  ACAAAATAGT  GAAATGGAGC  AAAAAGTAAA  ATCTTTAACC  CAAGTCTATG
2951  AGTCCAAACT  TGAAGATGGT  AACAAAGAAC  AGGAACAGAC  AAAGCAAATC
3001  TTGGTGGAAA  AGGAAAATAT  GATTTTACAA  ATGAGAGAAG  GACAGAAGAA
3051  AGAAATTGAG  ATACTCACAC  AGAAATTGTC  AGCCAAGGAG  GACAGTATTC
3101  ATATTTTGAA  TGAGGAATAT  GAAACCAAAT  TTAAAAACCA  AGAAAAAAAG
3151  ATGGAAAAAG  TTAAGCAGAA  AGCAAGGAG  ATGCAAGAAA  CGTTAAAGAA
3201  AAAATTACTG  GATCAGGAAG  CCAAACTTAA  GAAAGAGCTT  GAAAATACTG
3251  CTCTAGAGCT  TAGTCAGAAA  GAAAAACAGT  TTAATGCCAA  AATGCTGGAA
3301  ATGGCACAGG  CTAACTCAGC  TGGAATCAGT  GATGCAGTGT  CAAGACTGGA
3351  AACAAACCAA  AAAGAACAAA  TAGAAAGTCT  TACTGAGGTT  CATCGACGAG
3401  AACTCAATGA  TGTCATATCA  ATCTGGGAAA  AGAAACTTAA  TCAGCAAGCT
3451  GAAGAACTTC  AGGAAATACA  TGAAATCCAA  TTACAGGAAA  AAGAACAAGA
3501  GGTAGCAGAA  CTGAAACAAA  AGATCCTCCT  ATTTGGGTGT  GAAAAAGAAG
3551  AGATGAACAA  GGAAATAACA  TGGCTGAAGG  AAGAAGGTGT  TAAGCAGGAT
3601  ACAACATTAA  ATGAATTACA  GGAACAGTTA  AAGCAGAAGT  CTGCCCATGT
3651  GAATTCTCTT  GCACAAGATG  AAACTAAACT  GAAAGCTCAT  CTTGAAAAGC
3701  TAGAGGTTGA  CTTGAATAAG  TCTCTGAAGG  AAAATACTTT  TCTTCAAGAG
3751  CAGCTAGTTG  AACTGAAGAT  GCTGGCAGAA  GAAGATAAGC  GGAAGGTTTC
3801  TGAGTTGACT  AGCAAGTTGA  AAACCACAGA  TGAAGAATTC  CAGAGTTTGA
3851  AATCTTCACA  TGAAAAAGT  AACAAAAGCC  TAGAGGACAA  GAGCTTGGAA
3901  TTTAAAAAAC  TGTCTGAGGA  ACTAGCGATT  CAGCTAGATA  TTTGCTGTAA
3951  GAAAACCGAA  GCCTTATTAG  AAGCTAAAAC  AAATGAGCTA  ATCAACATTA
4001  GTAGTAGTAA  AACTAATGCC  ATTCTTTCTA  GGATTTCTCA  TTGTCAGCAC
4051  CGTACAACTA  AAGTTAAGGA  GGCACTGTTA  ATTAAAACTT  GCACAGTTTC
4101  TGAATTAGAA  GCACAACTTA  GACAGTTGAC  AGAGGAGCAA  AATACACTAA
4151  ATATTTCTTT  TCAACAGGCT  ACTCATCAGT  TAGAAGAAAA  AGAAAATCAA
4201  ATTAAGAGCA  TGAAGGCTGA  TATTGAAAGT  CTTGTAACAG  AAAAAGAAGC
4251  CTTACAGAAG  GAAGGAGGCA  ATCAGCAACA  GGCTGCTTCT  GAAAAGGAGT
4301  CTTGTATAAC  ACAGTTGAAG  AAAGAGTTAT  CTGAAAACAT  CAATGCTGTC
4351  ACATTGATGA  AAGAAGAGCT  TAAAGAAAAA  AAAGTTGAGA  TTAGCAGTCT
4401  TAGTAAACAA  CTAACTGATT  TGAATGTTCA  GCTTCAAAAT  AGCATCAGCC
4451  TATCCGAAAA  AGAAGCAGCC  ATTTCATCAC  TAAGAAAGCA  GTATGATGAA
4501  GAAAAATGTG  AATTGCTGGA  TCAGGTGCAA  GATTTATCTT  TTAAAGTTGA
4551  CACTCTGAGT  AAAGAGAAAA  TTTCTGCTCT  TGAGCAGGTA  GATGACTGGT
4601  CCAATAAATT  CTCAGAATGG  AAGAAGAAAG  CACAGTCAAG  ATTTACACAG
4651  CATCAAAACA  CTGTTAAAGA  ATTGCAGATC  CAGCTTGAGT  TAAAATCAAA
4701  GGAAGCTTAT  GAAAAGGATG  AGCAGATAAA  TTTATTGAAG  GAAGAGCTTG
4751  ATCAGCAAAA  TAAAGATTT  GATTGTTTAA  AGGGTGAAAT  GGAAGACGAC
4801  AAGAGCAAGA  TGGAGAAAAA  GGAGTCTAAT  TTAGAAACAG  AGTTAAAGTC
4851  TCAAACAGCA  AGAATTATGG  AATTAGAGGA  CCATATTACC  CAGAAAACTA
4901  TTGAAATAGA  GTCCTTAAAT  GAAGTTCTTA  AAAATTACAA  TCAACAAAAG
4951  GATATTGAAC  ACAAAGAATT  GGTTCAGAAA  CTTCAACATT  TTCAAGAGTT
5001  AGGAGAAGAA  AAGGACAACA  GGGTTAAAGA  AGCTGAAGAA  AAAATCTTAA
5051  CACTTGAAAA  CCAAGTTTAT  TCCATGAAAG  CTGAACTTGA  AACTAAGAAG
5101  AAAGAATTAG  AACATGTGAA  TTTAAGTGTG  AAAAGCAAAG  AGGAGGAGTT
5151  AAAGGCATTG  GAAGATAGGC  TTGAGTCAGA  AAGTGCTGCA  AAATTAGCAG
5201  AGTTGAAGAG  AAAAGCTGAA  CAAAAAATTG  CTGCCATTAA  GAAGCAGTTG
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5251   TTATCTCAAA TGGAAGAGAA AGAAGAACAG TATAAAAAAG GTACAGAAAG
5301   CCATTTGAGT GAGCTAAATA CAAAATTGCA GGAAAGAGAA AGGGAAGTTC
5351   ACATCTTGGA AGAAAAACTT AAGTCAGTGG AAAGTTCACA GTCAGAAACA
5401   TTAATTGTAC CCAGATCAGC AAAAAATGTG GCAGCATATA CTGAACAAGA
5451   AGAAGCAGAT TCCCAAGGCT GTGTGCAGAA GACATATGAA GAAAAAATCA
5501   GTGTTTTACA AAGAAACTTA ACTGAAAAAG AAAAGCTATT GCAGAGGGTA
5551   GGGCAGGAAA AAGAAGAGAC AGTTTCTTCT CATTTTGAAA TGCGATGCCA
5601   ATACCAGGAG CGCTTAATAA AGCTAGAACA TGCTGAGGCA AAGCAACATG
5651   AAGATCAAAG TATGATAGGT CATCTTCAAG AGGAGCTTGA AGAAAAAAAC
5701   AAGAAATATT CCTTGATAGT AGCCCAGCAT GTGGAAAAAG AAGGAGGTAA
5751   AAATAACATA CAGGCAAAGC AAAACTTGGA AAATGTGTTT GACGACGTCC
5801   AGAAAACCCT CCAGGAGAAG GAACTAACCT GTCAGATTTT GGAGCAAAAG
5851   ATAAAAGAGC TGGATTCCTG CTTAGTAAGA CAGAAAGAAG TACATAGAGT
5901   TGAAATGGAA GAGTTGACCT CAAAATATGA AAAATTACAG GCTTTACAAC
5951   AGATGGATGG AAGAAATAAA CCCACAGAAC TTTTGGAAGA AAACACTGAA
6001   GAAAGTCCA AATCACATTT GGTCCAACCC AAATTGCTTA GTAACATGGA
6051   AGCCCAGCAC AATGATCTGG AGTTTAAATT AGCCGGGGCA GAACGGGAGA
6101   AACAGAAACT GGGCAAGGAG ATTGTTAGAT TGCAGAAAGA CCTTCGAATG
6151   TTGAGAAAGG AGCATCAGCA AGAATTGGAA ATACTAAAGA AAGAATATGA
6201   TCAAGAAAGG GAAGAGAAAA TCAAACAGGA GCAGGAAGAT CTTGAACTGA
6251   AGCACAATTC CACATTAAAA CAGCTGATGA GGGAGTTTAA TACACAGCTG
6301   GCACAAAAGG AACAAGAGCT GGAAATGACC ATAAAAGAAA CTATCAATAA
6351   GGCCCAGGAG GTGGAGGCTG AACTTTTAGA AAGCCATCAA GAAGAGACAA
6401   ATCAGTTACT TAAAAAAATT GCTGAGAAAG ATGATGATCT AAAACGAACA
6451   GCCAAAAGAT ATGAAGAAAT CCTTGATGCT CGTGAAGAAG AAATGACTGC
6501   AAAAGTAAGG GACCTGCAGA CTCAACTTGA GGAGCTGCAG AAGAAATACC
6551   AGCAAAAGCT AGAGCAGGAG GAGAACCCTG GCAATGATAA TGTAACAATT
6601   ATGGAGCTAC AGACACAGCT AGCACAGAAG ACGACTTTAA TCAGTGATTC
6651   GAAATTGAAA GAGCAAGAGT TCAGAGAACA GATTCACAAT TTAGAAGACC
6701   GTTTGAAGAA ATATGAAAAG AATGTATATG CAACAACTGT GGGGACACCT
6751   TACAAAGGTG GCAATTTGTA CCATACGGAT GTCTCACTCT TTGGAGAACC
6801   TACCGAATTT GAGTATTTGC GAAAAGTGCT TTTTGAGTAT ATGATGGGTC
6851   GTGAGACTAA GACCATGGCA AAAGTTATAA CCACCGTACT GAAGTTCCCT
6901   GATGATCAGA CTCAGAAAAT TTTGGAAAGA GAAGATGCTC GGCTGATGTC
6951   ATGGCTCCGA TCTTCATCTT GAAGAAGAGT GACATTGGGT GACTGCTGCT
7001   TGGAAAACTG TCCACACTTG CTACTCTTTG AGAATGAAGT TGTCATTCAG
7051   GGCCCCTCAT GTAGCCAAAA GACCAAGAAA AATCTGGCCC ACAGATAAGT
7101   TGCAGACTGC CTTTAAAATA GATTTTATCA GTGGAGAAAT GGTGATAGTT
7151   TTTTCTTCAG TTTTCTCTTG GGAAGAGTTT TATGTTGTTT AAAAGATATT
7201   TTGATAACTT AACCTGCTTT ATGGGCTTAC ATAATATTCC TTTCATCCAT
7251   TCTTTTTAAA GAACGGCTTA CCTTTCCTAT TTATTTTTAG GGTGATTTTT
7301   TAAAAGACT TGTGCAATAC ATTTTGAGGT GAAACTTAGT GGATTTTTTC
7351   TGATAAATTA GAGCATTTAA TTGACTATTT TATTCAGGTT GATCTGTTGA
7401   ATATTTGCTA AAGACCAGTT CTTTAAGCTA AGACATGTAA AAAATCCCAA
7451   ATGGCAGTAC CTCATTGTTT ACTTAGCTTT TGTACTTATA TTTTTCAGAG
7501   GAAAAAACAC TACTGTAAAT TGTGAATAGC CAATACATAA CTGTATTGTA
7551   TGCAAATCTG TGATTGTTGG CAGTGTCATC TCTGAGAAAC AGATAAATAA
7601   AGTTTATTTA CTATATAACC AAAAAAAAAA AAAAAA
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Fig. 7: SEQ ID NO. 4: amino acid sequence of human golgin-245, splice variant 2 (GenBank accession number Q13439)

Length: 2230 aa

```
   1   MFKKLKQKIS EEQQQLQQAL APAQASSNSS TPTRMRSRTS SFTEQLDEGT
  51   PNRESGDTQS FAQKLQLRVP SVESLFRSPI KESLFRSSSK ESLVRTSSRE
 101   SLNRLDLDSS TASFDPPSDM DSEAEDLVGN SDSLNKEQLI QRLRRMERSL
 151   SSYRGKYSEL VTAYQMLQRE KKKLQGILSQ SQDKSLRRIA ELREELQMDQ
 201   QAKKHLQEEF DASLEEKDQY ISVLQTQVSL LKQRLRNGPM NVDVLKPLPQ
 251   LEPQAEVFTK EENPESDGEP VVEDGTSVKT LETLQQRVKR QENLLKRCKE
 301   TIQSHKEQCT LLTSEKEALQ EQLDERLQEL EKIKDLHMAE KTKLITQLRD
 351   AKNLIEQLEQ DKGMVIAETK RQMHETLEMK EEEIAQLRSR IKQMTTQGEE
 401   LREQKEKSER AAFEELEKAL STAQKTEEAR RKLKAEMDEQ IKTIEKTSEE
 451   ERISLQQELS RVKQEVVDVM KKSSEEQIAK LQKLHEKELA RKEQELTKKL
 501   QTREREFQEQ MKVALEKSQS EYLKISQEKE QQESLALEEL ELQKKAILTE
 551   SENKLRDLQQ EAETYRTRIL ELESSLEKSL QENKNQSKDL AVHLEAEKNK
 601   HNKEITVMVE KHKTELESLK HQQDALWTEK LQVLKQQYQT EMEKLREKCE
 651   QEKETLLKDK EIIFQAHIEE MNEKTLEKLD VKQTELESLS SELSEVLKAR
 701   HKLEEELSVL KDQTDKMKQE LEAKMDEQKN HHQQQVDSII KEHEVSIQRT
 751   EKALKDQINQ LELLLKERDK HLKEHQAHVE NLEADIKRSE GELQQASAKL
 801   DVFQSYQSAT HEQTKAYEEQ LAQLQQKLLD LETERILLTK QVAEVEAQKK
 851   DVCTELDAHK IQVQDLMQQL EKQNSEMEQK VKSLTQVYES KLEDGNKEQE
 901   QTKQILVEKE NMILQMREGQ KKEIEILTQK LSAKEDSIHI LNEEYETKFK
 951   NQEKKMEKVK QKAKEMQETL KKKLLDQEAK LKKELENTAL ELSQKEKQFN
1001   AKMLEMAQAN SAGISDAVSR LETNQKEQIE SLTEVHRREL NDVISIWEKK
1051   LNQQAEELQE IHEIQLQEKE QEVAELKQKI LLFGCEKEEM NKEITWLKEE
1101   GVKQDTTLNE LQEQLKQKSA HVNSLAQDET KLKAHLEKLE VDLNKSLKEN
1151   TFLQEQLVEL KMLAEEDKRK VSELTSKLKT TDEEFQSLKS SHEKSNKSLE
1201   DKSLEFKKLS EELAIQLDIC CKKTEALLEA KTNELINISS SKTNAILSRI
1251   SHCQHRTTKV KEALLIKTCT VSELEAQLRQ LTEEQNTLNI SFQQATHQLE
1301   EKENQIKSMK ADIESLVTEK EALQKEGGNQ QQAASEKESC ITQLKKELSE
1351   NINAVTLMKE ELKEKKVEIS SLSKQLTDLN VQLQNSISLS EKEAAISSLR
1401   KQYDEEKCEL LDQVQDLSFK VDTLSKEKIS ALEQVDDWSN KFSEWKKKAQ
1451   SRFTQHQNTV KELQIQLELK SKEAYEKDEQ INLLKEELDQ QNKRFDCLKG
1501   EMEDDKSKME KKESNLETEL KSQTARIMEL EDHITQKTIE IESLNEVLKN
1551   YNQQKDIEHK ELVQKLQHFQ ELGEEKDNRV KEAEEKILTL ENQVYSMKAE
1601   LETKKKELEH VNLSVKSKEE ELKALEDRLE SESAAKLAEL KRKAEQKIAA
1651   IKKQLLSQME EKEEQYKKGT ESHLSELNTK LQEREREVHI LEEKLKSVES
1701   SQSETLIVPR SAKNVAAYTE QEEADSQGCV QKTYEEKISV LQRNLTEKEK
1751   LLQRVGQEKE ETVSSHFEMR CQYQERLIKL EHAEAKQHED QSMIGHLQEE
1801   LEEKNKKYSL IVAQHVEKEG GKNNIQAKQN LENVFDDVQK TLQEKELTCQ
1851   ILEQKIKELD SCLVRQKEVH RVEMEELTSK YEKLQALQQM DGRNKPTELL
1901   EENTEEKSKS HLVQPKLLSN MEAQHNDLEF KLAGAEREKQ KLGKEIVRLQ
1951   KDLRMLRKEH QQELEILKKE YDQEREEKIK QEQEDLELKH NSTLKQLMRE
2001   FNTQLAQKEQ ELEMTIKETI NKAQEVEAEL LESHQEETNQ LLKKIAEKDD
2051   DLKRTAKRYE EILDAREEEM TAKVRDLQTQ LEELQKKYQQ KLEQEENPGN
2101   DNVTIMELQT QLAQKTTLIS DSKLKEQEFR EQIHNLEDRL KKYEKNVYAT
2151   TVGTPYKGGN LYHTDVSLFG EPTEFEYLRK VLFEYMMGRE TKTMAKVITT
2201   VLKFPDDQTQ KILEREDARL MFTSPRSGIF
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Fig. 8: SEQ ID NO. 5: nucleotide sequence of human golgin-245 cDNA, splice variant 2 (GenBank accession number U41740)

Length: 7695 bp

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   1  GCAACGAAGG  TACCATGGCC  GTTGTCGTCG  CCGCCGCGGC  TCCCGGGGCT
  51  GGATGGGGGG  CCGAGGCCAG  CCAGTGGCAC  CCGGAAGAAA  GAGACGCGGC
 101  GGCGGCGACG  CCGACACCCT  CAGGACGAGT  GTCCGGACTT  GCCCACAGCC
 151  TCAAGGAGGA  GACGGCGAGG  CCCGGCCCCC  GCTGTCCCTG  GTGTAAAGAA
 201  GTCGCCGTAG  CCGTCGCGGC  CGGGACTCCC  CGGGCTCTCG  CCCTTCAGGT
 251  TTCGTTGACA  CTCAGGACCG  TACGTACGCT  GCGCCATGTT  CAAGAAACTG
 301  AAGCAAAAGA  TCAGCGAGGA  GCAGCAGCAG  CTCCAGCAGG  CGCTGGCTCC
 351  TGCTCAGGCG  TCCTCCAATT  CTTCAACACC  AACAAGAATG  AGGAGCAGGA
 401  CATCTTCATT  TACAGAGCAA  CTTGATGAAG  GTACACCCAA  TAGAGAGTCA
 451  GGTGACACAC  AGTCTTTTGC  ACAGAAGCTC  CAGCTCCGGG  TGCCCTCCGT
 501  GGAGTCTTTG  TTTCGAAGTC  CGATAAAGGA  ATCTCTATTC  CGGTCTTCTT
 551  CTAAAGAGTC  TTTGGTACGA  ACATCTTCCA  GAGAATCCCT  GAATCGACTT
 601  GACCTGGACA  GTTCTACTGC  CAGTTTTGAT  CCACCCTCTG  ATATGGATAG
 651  CGAGGCTGAA  GACTTGGTAG  GGAATTCAGA  CAGTCTCAAC  AAAGAACAGT
 701  TGATTCAGCG  GTTGCGAAGA  ATGGAACGAA  GCTTAAGTAG  CTACAGGGGA
 751  AAATATTCTG  AGCTTGTTAC  AGCTTATCAG  ATGCTTCAGA  GAGAGAAGAA
 801  AAAGCTACAA  GGTATATTAA  GTCAGAGTCA  GGATAAATCA  CTTCGGAGAA
 851  TAGCAGAATT  AAGAGAGGAG  CTCCAAATGG  ACCAGCAGGC  AAAGAAACAT
 901  CTGCAAGAGG  AGTTTGATGC  ATCTTTAGAG  GAGAAAGATC  AGTATATCAG
 951  TGTTCTCCAA  ACTCAGGTTT  CTCTACTGAA  ACAACGATTA  CGAAATGGCC
1001  CGATGAATGT  TGATGTACTG  AAACCACTTC  CTCAGCTGGA  ACCACAGGCT
1051  GAAGTCTTCA  CTAAAGAAGA  GAATCCAGAA  AGTGATGGAG  AGCCAGTAGT
1101  GGAAGATGGA  ACTTCTGTAA  AAACACTGGA  AACACTCCAG  CAAAGAGTGA
1151  AGCGTCAAGA  GAACCTACTT  AAGCGTTGTA  AGGAAACAAT  TCAGTCACAT
1201  AAGGAACAAT  GTACACTATT  AACTAGTGAA  AAAGAAGCTC  TGCAAGAACA
1251  ACTGGATGAA  AGACTTCAAG  AACTAGAAAA  GATAAAGGAC  CTTCATATGG
1301  CCGAGAAGAC  TAAACTTATC  ACTCAGTTGC  GTGATGCAAA  GAACTTAATT
1351  GAACAGCTTG  AACAAGATAA  GGGAATGGTA  ATCGCAGAGA  CAAAACGTCA
1401  GATGCATGAA  ACCCTGGAAA  TGAAAGAAGA  AGAAATTGCT  CAACTCCGTA
1451  GTCGCATCAA  ACAGATGACT  ACCCAGGGAG  AGGAATTACG  GAACAGAAA
1501  GAAAAGTCCG  AAAGAGCTGC  TTTTGAGGAA  CTTGAAAAAG  CTTTGAGTAC
1551  AGCCCAAAAA  ACAGAGGAAG  CACGGAGAAA  ACTGAAGGCA  GAAATGGATG
1601  AACAAATAAA  AACTATCGAA  AAAACAAGTG  AGGAGGAACG  CATCAGTCTT
1651  CAACAGGAAT  TAAGTCGGGT  GAAACAGGAG  GTTGTTGATG  TAATGAAAAA
1701  ATCCTCAGAA  GAACAAATTG  CTAAGCTACA  GAAGCTTCAT  GAAAAGGAGC
1751  TGGCCAGAAA  AGAGCAGGAA  CTGACCAAGA  AGCTTCAGAC  CCGAGAAAGG
1801  GAATTTCAGG  AACAAATGAA  AGTAGCTCTT  GAAAAGAGTC  AATCAGAATA
1851  TTTGAAGATC  AGCCAAGAAA  AGAACAGCA  AGAATCTTTG  GCCCTAGAAG
1901  AGTTAGAGTT  GCAGAAAAAA  GCAATCCTCA  CAGAAAGTGA  AAATAAACTT
1951  CGGGACCTTC  AGCAAGAAGC  AGAGACTTAC  AGAACTAGAA  TTCTTGAATT
2001  GGAAAGTTCT  TTGGAAAAAA  GCTTACAAGA  AAACAAAAAT  CAGTCAAAAG
2051  ATTTGGCTGT  TCATCTGGAA  GCTGAAAAAA  ATAAGCACAA  TAAGGAGATT
2101  ACAGTCATGG  TTGAAAAACA  CAAGACAGAA  TTGGAAAGCC  TTAAGCATCA
2151  GCAGGATGCC  CTTTGGACTG  AAAAACTCCA  AGTCTTAAAG  CAACAATATC
2201  AGACTGAAAT  GGAAAAACTT  AGGGAAAAGT  GTGAACAAGA  AAAAGAAACA
2251  TTGTTGAAAG  ACAAAGAGAT  TATCTTCCAG  GCCCACATAG  AAGAAATGAA
2301  TGAAAAGACT  TTAGAAAGC  TTGATGTGAA  GCAAACAGAA  CTAGAATCAT
2351  TATCTTCTGA  ACTGTCAGAA  GTATTAAAAG  CCCGTCACAA  ACTAGAAGAG
2401  GAACTTTCTG  TTCTGAAAGA  TCAAACAGAT  AAAATGAAGC  AGGAATTAGA
2451  GGCCAAGATG  GATGAACAGA  AAAATCATCA  CCAGCAGCAA  GTTGACAGTA
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2501  TCATTAAAGA ACACGAGGTA TCTATCCAGA GGACTGAGAA GGCATTAAAA
2551  GATCAAATTA ATCAACTTGA GCTTCTCTTG AAGGAAAGGG ACAAGCATTT
2601  GAAAGAGCAT CAGGCTCATG TAGAAAATTT AGAGGCAGAT ATTAAAAGGT
2651  CTGAAGGGGA ACTCCAGCAG GCATCTGCTA AGCTGGACGT TTTTCAGTCT
2701  TACCAGAGTG CCACACATGA GCAGACAAAA GCATATGAGG AACAGTTGGC
2751  CCAATTGCAG CAGAAGTTGT TGGATTTGGA AACAGAAAGA ATTCTTCTTA
2801  CCAAACAGGT TGCTGAAGTT GAAGCACAAA AGAAAGATGT TTGTACTGAG
2851  TTAGATGCTC ACAAAATCCA GGTGCAGGAC TTAATGCAGC AACTTGAAAA
2901  ACAAAATAGT GAAATGGAGC AAAAAGTAAA ATCTTTAACC CAAGTCTATG
2951  AGTCCAAACT TGAAGATGGT AACAAAGAAC AGGAACAGAC AAAGCAAATC
3001  TTGGTGGAAA AGGAAAATAT GATTTTACAA ATGAGAGAAG GACAGAAGAA
3051  AGAAATTGAG ATACTCACAC AGAAATTGTC AGCCAAGGAG GACAGTATTC
3101  ATATTTTGAA TGAGGAATAT GAAACCAAAT TTAAAAACCA AGAAAAAAAG
3151  ATGGAAAAAG TTAAGCAGAA AGCAAGGAG ATGCAAGAAA CGTTAAAGAA
3201  AAAATTACTG GATCAGGAAG CCAAACTTAA GAAAGAGCTT GAAAATACTG
3251  CTCTAGAGCT TAGTCAGAAA GAAAAACAGT TTAATGCCAA AATGCTGGAA
3301  ATGGCACAGG CTAACTCAGC TGGAATCAGT GATGCAGTGT CAAGACTGGA
3351  AACAAACCAA AAAGAACAAA TAGAAAGTCT TACTGAGGTT CATCGACGAG
3401  AACTCAATGA TGTCATATCA ATCTGGGAAA AGAAACTTAA TCAGCAAGCT
3451  GAAGAACTTC AGGAAATACA TGAAATCCAA TTACAGGAAA AAGAACAAGA
3501  GGTAGCAGAA CTGAAACAAA AGATCCTCCT ATTTGGGTGT GAAAAAGAAG
3551  AGATGAACAA GGAAATAACA TGGCTGAAGG AAGAAGGTGT TAAGCAGGAT
3601  ACAACATTAA ATGAATTACA GGAACAGTTA AAGCAGAAGT CTGCCCATGT
3651  GAATTCTCTT GCACAAGATG AAACTAAACT GAAAGCTCAT CTTGAAAAGC
3701  TAGAGGTTGA CTTGAATAAG TCTCTGAAGG AAAATACTTT TCTTCAAGAG
3751  CAGCTAGTTG AACTGAAGAT GCTGGCAGAA GAAGATAAGC GGAAGGTTTC
3801  TGAGTTGACT AGCAAGTTGA AAACCACAGA TGAAGAATTC CAGAGTTTGA
3851  AATCTTCACA TGAAAAAAGT AACAAAGCC TAGAGGACAA GAGCTTGGAA
3901  TTTAAAAAAC TGTCTGAGGA ACTAGCGATT CAGCTAGATA TTTGCTGTAA
3951  GAAAACCGAA GCCTTATTAG AAGCTAAAAC AAATGAGCTA ATCAACATTA
4001  GTAGTAGTAA AACTAATGCC ATTCTTTCTA GGATTTCTCA TTGTCAGCAC
4051  CGTACAACTA AAGTTAAGGA GGCACTGTTA ATTAAAACTT GCACAGTTTC
4101  TGAATTAGAA GCACAACTTA GACAGTTGAC AGAGGAGCAA AATACACTAA
4151  ATATTTCTTT TCAACAGGCT ACTCATCAGT TAGAAGAAAA AGAAAATCAA
4201  ATTAAGAGCA TGAAGGCTGA TATTGAAAGT CTTGTAACAG AAAAAGAAGC
4251  CTTACAGAAG GAAGGAGGCA ATCAGCAACA GGCTGCTTCT GAAAAGGAGT
4301  CTTGTATAAC ACAGTTGAAG AAAGAGTTAT CTGAAAACAT CAATGCTGTC
4351  ACATTGATGA AGAAGAGCT TAAAGAAAAA AAAGTTGAGA TTAGCAGTCT
4401  TAGTAAACAA CTAACTGATT TGAATGTTCA GCTTCAAAAT AGCATCAGCC
4451  TATCCGAAAA AGAAGCAGCC ATTTCATCAC TAAGAAAGCA GTATGATGAA
4501  GAAAAATGTG AATTGCTGGA TCAGGTGCAA GATTTATCTT TTAAAGTTGA
4551  CACTCTGAGT AAAGAGAAAA TTTCTGCTCT TGAGCAGGTA GATGACTGGT
4601  CCAATAAATT CTCAGAATGG AAGAAGAAAG CACAGTCAAG ATTTACACAG
4651  CATCAAAACA CTGTTAAAGA ATTGCAGATC CAGCTTGAGT TAAAATCAAA
4701  GGAAGCTTAT GAAAAGGATG AGCAGATAAA TTTATTGAAG GAAGAGCTTG
4751  ATCAGCAAAA TAAAGATTT GATTGTTTAA AGGGTGAAAT GGAAGACGAC
4801  AAGAGCAAGA TGGAGAAAAA GGAGTCTAAT TTAGAAACAG AGTTAAAGTC
4851  TCAAACAGCA AGAATTATGG AATTAGAGGA CCATATTACC CAGAAAACTA
4901  TTGAAATAGA GTCCTTAAAT GAAGTTCTTA AAAATTACAA TCAACAAAAG
4951  GATATTGAAC ACAAAGAATT GGTTCAGAAA CTTCAACATT TTCAAGAGTT
5001  AGGAGAAGAA AAGGACAACA GGGTTAAAGA AGCTGAAGAA AAAATCTTAA
5051  CACTTGAAAA CCAAGTTTAT CCATGAAAG CTGAACTTGA AACTAAGAAG
5101  AAAGAATTAG AACATGTGAA TTTAAGTGTG AAAAGCAAAG AGGAGGAGTT
5151  AAAGGCATTG GAAGATAGGC TTGAGTCAGA AAGTGCTGCA AAATTAGCAG
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5201  AGTTGAAGAG AAAAGCTGAA CAAAAAATTG CTGCCATTAA GAAGCAGTTG
5251  TTATCTCAAA TGGAAGAGAA AGAAGAACAG TATAAAAAAG GTACAGAAAG
5301  CCATTTGAGT GAGCTAAATA CAAAATTGCA GGAAAGAGAA AGGGAAGTTC
5351  ACATCTTGGA AGAAAAACTT AAGTCAGTGG AAAGTTCACA GTCAGAAACA
5401  TTAATTGTAC CCAGATCAGC AAAAAATGTG GCAGCATATA CTGAACAAGA
5451  AGAAGCAGAT TCCCAAGGCT GTGTGCAGAA GACATATGAA GAAAAAATCA
5501  GTGTTTTACA AAGAAACTTA ACTGAAAAAG AAAAGCTATT GCAGAGGGTA
5551  GGGCAGGAAA AAGAAGAGAC AGTTTCTTCT CATTTTGAAA TGCGATGCCA
5601  ATACCAGGAG CGCTTAATAA AGCTAGAACA TGCTGAGGCA AAGCAACATG
5651  AAGATCAAAG TATGATAGGT CATCTTCAAG AGGAGCTTGA AGAAAAAAAC
5701  AAGAAATATT CCTTGATAGT AGCCCAGCAT GTGGAAAAAG AAGGAGGTAA
5751  AAATAACATA CAGGCAAAGC AAAACTTGGA AAATGTGTTT GACGACGTCC
5801  AGAAAACCCT CCAGGAGAAG GAACTAACCT GTCAGATTTT GGAGCAAAAG
5851  ATAAAGAGC TGGATTCCTG CTTAGTAAGA CAGAAGAAG TACATAGAGT
5901  TGAAATGGAA GAGTTGACCT CAAAATATGA AAAATTACAG GCTTTACAAC
5951  AGATGGATGG AAGAAATAAA CCCACAGAAC TTTTGGAAGA AAACACTGAA
6001  GAAAAGTCCA AATCACATTT GGTCCAACCC AAATTGCTTA GTAACATGGA
6051  AGCCCAGCAC AATGATCTGG AGTTTAAATT AGCCGGGGCA GAACGGGAGA
6101  AACAGAAACT GGGCAAGGAG ATTGTTAGAT TGCAGAAAGA CCTTCGAATG
6151  TTGAGAAAGG AGCATCAGCA AGAATTGGAA ATACTAAAGA AAGAATATGA
6201  TCAAGAAAGG GAAGAGAAAA TCAAACAGGA GCAGGAAGAT CTTGAACTGA
6251  AGCACAATTC CACATTAAAA CAGCTGATGA GGGAGTTTAA TACACAGCTG
6301  GCACAAAAGG AACAAGAGCT GGAAATGACC ATAAAAGAAA CTATCAATAA
6351  GGCCCAGGAG GTGGAGGCTG AACTTTTAGA AAGCCATCAA GAAGAGACAA
6401  ATCAGTTACT TAAAAAAATT GCTGAGAAAG ATGATGATCT AAAACGAACA
6451  GCCAAAAGAT ATGAAGAAAT CCTTGATGCT CGTGAAGAAG AAATGACTGC
6501  AAAAGTAAGG GACCTGCAGA CTCAACTTGA GGAGCTGCAG AAGAAATACC
6551  AGCAAAAGCT AGAGCAGGAG GAGAACCCTG GCAATGATAA TGTAACAATT
6601  ATGGAGCTAC AGACACAGCT AGCACAGAAG ACGACTTTAA TCAGTGATTC
6651  GAAATTGAAA GAGCAAGAGT TCAGAGAACA GATTCACAAT TTAGAAGACC
6701  GTTTGAAGAA ATATGAAAG AATGTATATG CAACAACTGT GGGGACACCT
6751  TACAAAGGTG GCAATTTGTA CCATACGGAT GTCTCACTCT TTGGAGAACC
6801  TACCGAATTT GAGTATTTGC GAAAAGTGCT TTTTGAGTAT ATGATGGGTC
6851  GTGAGACTAA GACCATGGCA AAAGTTATAA CCACCGTACT GAAGTTCCCT
6901  GATGATCAGA CTCAGAAAAT TTTGGAAAGA GAAGATGCTC GGCTGATGTT
6951  TACTTCACCT CGCAGTGGTA TCTTCTGAGT AAACCATCAG TCTGTGCTTA
7001  GTTAACATGT GTCATGGCTC CGATCTTCAT CTTGAAGAAG AGTGACATTG
7051  GGTGACTGCT GCTTGGAAAA CTGTCCACAC TTGCTACTCT TTGAGAATGA
7101  AGTTGTCATT CAGGGCCCCT CATGTAGCCA AAAGACCAAG AAAAATCTGG
7151  CCCACAGATA AGTTGCAGAC TGCCTTTAAA ATAGATTTTA TCAGTGGAGA
7201  AATGGTGATA GTTTTTTCTT CAGTTTTCTC TTGGGAAGGA GTTTTATGTT
7251  GTTTAAAAGA TATTTTGATA ACTTAACCTG CTTTATGGGC TTACATAATA
7301  TTCCTTTCAT CCATTCTTTT TAAAGAACGG CTTACCTTTC CTATTTATTT
7351  TTAGGGTGAT TTTTTAAAAA GACTTGTGCA ATACATTTTG AGGTGAAACT
7401  TAGTGGATTT TTTCTGATAA ATTAGAGCAT TTAATTGACT ATTTTATTCA
7451  GGTTGATCTG TTGAATATTT GCTAAAGACC AGTTCTTTAA GCTAAGACAT
7501  GTAAAAAATC CCAAATGGCA GTACCTCATT GTTTACTTAG CTTTTGTACT
7551  TATATTTTTC AGAGGAAAAA ACACTACTGT AAATTGTGAA TAGCCAATAC
7601  ATAACTGTAT TGTATGCAAA TCTGTGATTG TTGGCAGTGT CATCTCTGAG
7651  AAACAGATAA ATAAAGTTTA TTTACTATAA AAAAAAAAAA AAAAG
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Fig. 9: SEQ ID NO. 6:amino acid sequence of human golgin-245, splice variant 3

Length: 2250 aa

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   1  MFKKLKQKIS EEQQQLQQAL APAQASSNSS TPTRMRSRTS SFTEQLDEGT
  51  PNRENASTHA SKSPDSVNGS EPSIPQSGDT QSFAQKLQLR VPSVESLFRS
 101  PIKESLFRSS SKESLVRTSS RESLNRLDLD SSTASFDPPS DMDSEAEDLV
 151  GNSDSLNKEQ LIQRLRRMER SLSSYRGKYS ELVTAYQMLQ REKKKLQGIL
 201  SQSQDKSLRR IAELREELQM DQQAKKHLQE EFDASLEEKD QYISVLQTQV
 251  SLLKQRLRNG PMNVDVLKPL PQLEPQAEVF TKEENPESDG EPVVEDGTSV
 301  KTLETLQQRV KRQENLLKRC KETIQSHKEQ CTLLTSEKEA LQEQLDERLQ
 351  ELEKIKDLHM AEKTKLITQL RDAKNLIEQL EQDKGMVIAE TKRQMHETLE
 401  MKEEEIAQLR SRIKQMTTQG EELREQKEKS ERAAFEELEK ALSTAQKTEE
 451  ARRKLKAEMD EQIKTIEKTS EEERISLQQE LSRVKQEVVD VMKKSSEEQI
 501  AKLQKLHEKE LARKEQELTK KLQTREREFQ EQMKVALEKS QSEYLKISQE
 551  KEQQESLALE ELELQKKAIL TESENKLRDL QQEAETYRTR ILELESSLEK
 601  SLQENKNQSK DLAVHLEAEK NKHNKEITVM VEKHKTELES LKHQQDALWT
 651  EKLQVLKQQY QTEMEKLREK CEQEKETLLK DKEIIFQAHI EEMNEKTLEK
 701  LDVKQTELES LSSELSEVLK ARHKLEEELS VLKDQTDKMK QELEAKMDEQ
 751  KNHHQQQVDS IIKEHEVSIQ RTEKALKDQI NQLELLLKER DKHLKEHQAH
 801  VENLEADIKR SEGELQQASA KLDVFQSYQS ATHEQTKAYE EQLAQLQQKL
 851  LDLETERILL TKQVAEVEAQ KKDVCTELDA HKIQVQDLMQ QLEKQNSEME
 901  QKVKSLTQVY ESKLEDGNKE QEQTKQILVE KENMILQMRE GQKKEIEILT
 951  QKLSAKEDSI HILNEEYETK FKNQEKKMEK VKQKAKEMQE TLKKKLLDQE
1001  AKLKKELENT ALELSQKEKQ FNAKMLEMAQ ANSAGISDAV SRLETNQKEQ
1051  IESLTEVHRR ELNDVISIWE KKLNQQAEEL QEIHEIQLQE KEQEVAELKQ
1101  KILLFGCEKE EMNKEITWLK EEGVKQDTTL NELQEQLKQK SAHVNSLAQD
1151  ETKLKAHLEK LEVDLNKSLK ENTFLQEQLV ELKMLAEEDK RKVSELTSKL
1201  KTTDEEFQSL KSSHEKSNKS LEDKSLEFKK LSEELAIQLD ICCKKTEALL
1251  EAKTNELINI SSSKTNAILS RISHCQHRTT KVKEALLIKT CTVSELEAQL
1301  RQLTEEQNTL NISFQQATHQ LEEKENQIKS MKADIESLVT EKEALQKEGG
1351  NQQQAASEKE SCITQLKKEL SENINAVTLM KEELKEKKVE ISSLSKQLTD
1401  LNVQLQNSIS LSEKEAAISS LRKQYDEEKC ELLDQVQDLS FKVDTLSKEK
1451  ISALEQVDDW SNKFSEWKKK AQSRFTQHQN TVKELQIQLE LKSKEAYEKD
1501  EQINLLKEEL DQQNKRFDCL KGEMEDDKSK MEKKESNLET ELKSQTARIM
1551  ELEDHITQKT IEIESLNEVL KNYNQQKDIE HKELVQKLQH FQELGEEKDN
1601  RVKEAEEKIL TLENQVYSMK AELETKKKEL EHVNLSVKSK EEELKALEDR
1651  LESESAAKLA ELKRKAEQKI AAIKKQLLSQ MEEKEEQYKK GTESHLSELN
1701  TKLQEREREV HILEEKLKSV ESSQSETLIV PRSAKNVAAY TEQEEADSQG
1751  CVQKTYEEKI SVLQRNLTEK EKLLQRVGQE KEETVSSHFE MRCQYQERLI
1801  KLEHAEAKQH EDQSMIGHLQ EELEEKNKKY SLIVAQHVEK EGGKNNIQAK
1851  QNLENVFDDV QKTLQEKELT CQILEQKIKE LDSCLVRQKE VHRVEMEELT
1901  SKYEKLQALQ QMDGRNKPTE LLEENTEEKS KSHLVQPKLL SNMEAQHNDL
1951  EFKLAGAERE KQKLGKEIVR LQKDLRMLRK EHQQELEILK KEYDQEREEK
2001  IKQEQEDLEL KHNSTLKQLM REFNTQLAQK EQELEMTIKE TINKAQEVEA
2051  ELLESHQEET NQLLKKIAEK DDDLKRTAKR YEEILDAREE EMTAKVRDLQ
2101  TQLEELQKKY QQKLEQEENP GNDNVTIMEL QTQLAQKTTL ISDSKLKEQE
2151  FREQIHNLED RLKKYEKNVY ATTVGTPYKG GNLYHTDVSL FGEPTEFEYL
2201  RKVLFEYMMG RETKTMAKVI TTVLKFPDDQ TQKILEREDA RLMSWLRSSS
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Fig. 10: SEQ ID NO. 7: nucleotide sequence of human golgin-245 cDNA, splice variant 3

Length: 7743 bp

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   1  GCAACGAAGG TACCATGGCC GTTGTCGTCG CCGCCGCGGC TCCCGGGGCT
  51  GGATGGGGGG CCGAGGCCAG CCAGTGGCAC CCGGAAGAAA GAGACGCGGC
 101  GGCGGCGACG CCGACACCCT CAGGACGAGT GTCCGGACTT GCCCACAGCC
 151  TCAAGGAGGA GACGGCGAGG CCCGGCCCCC GCTGTCCCTG GTGTAAAGAA
 201  GTCGCCGTAG CCGTCGCGGC CGGGACTCCC CGGGCTCTCG CCCTTCAGGT
 251  TTCGTTGACA CTCAGGACCG TACGTACGCT GCGCCATGTT CAAGAAACTG
 301  AAGCAAAAGA TCAGCGAGGA GCAGCAGCAG CTCCAGCAGG CGCTGGCTCC
 351  TGCTCAGGCG TCCTCCAATT CTTCAACACC AACAAGAATG AGGAGCAGGA
 401  CATCTTCATT TACAGAGCAA CTTGATGAAG GTACACCCAA TAGAGAGAAT
 451  GCATCTACTC ATGCCTCGAA ATCTCCTGAC AGTGTTAATG GAAGTGAACC
 501  AAGCATTCCT CAGTCAGGTG ACACACAGTC TTTTGCACAG AAGCTCCAGC
 551  TCCGGGTGCC CTCCGTGGAG TCTTTGTTTC GAAGTCCGAT AAAGGAATCT
 601  CTATTCCGGT CTTCTTCTAA AGAGTCTTTG GTACGAACAT CTTCCAGAGA
 651  ATCCCTGAAT CGACTTGACC TGGACAGTTC TACTGCCAGT TTTGATCCAC
 701  CCTCTGATAT GGATAGCGAG GCTGAAGACT TGGTAGGGAA TTCAGACAGT
 751  CTCAACAAAG AACAGTTGAT TCAGCGGTTG CGAAGAATGG AACGAAGCTT
 801  AAGTAGCTAC AGGGGAAAAT ATTCTGAGCT TGTTACAGCT TATCAGATGC
 851  TTCAGAGAGA GAAGAAAAAG CTACAAGGTA TATTAAGTCA GAGTCAGGAT
 901  AAATCACTTC GGAGAATAGC AGAATTAAGA GAGGAGCTCC AAATGGACCA
 951  GCAGGCAAAG AAACATCTGC AAGAGGAGTT TGATGCATCT TTAGAGGAGA
1001  AAGATCAGTA TATCAGTGTT CTCCAAACTC AGGTTTCTCT ACTGAAACAA
1051  CGATTACGAA ATGGCCCGAT GAATGTTGAT GTACTGAAAC CACTTCCTCA
1101  GCTGGAACCA CAGGCTGAAG TCTTCACTAA AGAAGAGAAT CCAGAAAGTG
1151  ATGGAGAGCC AGTAGTGGAA GATGGAACTT CTGTAAAAAC ACTGGAAACA
1201  CTCCAGCAAA GAGTGAAGCG TCAAGAGAAC CTACTTAAGC GTTGTAAGGA
1251  AACAATTCAG TCACATAAGG AACAATGTAC ACTATTAACT AGTGAAAAAG
1301  AAGCTCTGCA AGAACAACTG GATGAAAGAC TTCAAGAACT AGAAAAGATA
1351  AAGGACCTTC ATATGGCCGA GAAGACTAAA CTTATCACTC AGTTGCGTGA
1401  TGCAAAGAAC TTAATTGAAC AGCTTGAACA AGATAAGGGA ATGGTAATCG
1451  CAGAGACAAA ACGTCAGATG CATGAAACCC TGGAAATGAA AGAAGAAGAA
1501  ATTGCTCAAC TCCGTAGTCG CATCAAACAG ATGACTACCC AGGGAGAGGA
1551  ATTACGGGAA CAGAAAGAAA AGTCCGAAAG AGCTGCTTTT GAGGAACTTG
1601  AAAAAGCTTT GAGTACAGCC CAAAAAACAG AGGAAGCACG GAGAAAACTG
1651  AAGGCAGAAA TGGATGAACA AATAAAAACT ATCGAAAAAA CAAGTGAGGA
1701  GGAACGCATC AGTCTTCAAC AGGAATTAAG TCGGGTGAAA CAGGAGGTTG
1751  TTGATGTAAT GAAAAAATCC TCAGAAGAAC AAATTGCTAA GCTACAGAAG
1801  CTTCATGAAA AGGAGCTGGC CAGAAAGAG CAGGAACTGA CCAAGAAGCT
1851  TCAGACCCGA GAAAGGGAAT TCAGGAACA AATGAAAGTA GCTCTTGAAA
1901  AGAGTCAATC AGAATATTTG AAGATCAGCC AAGAAAAAGA ACAGCAAGAA
1951  TCTTTGGCCC TAGAAGAGTT AGAGTTGCAG AAAAAAGCAA TCCTCACAGA
2001  AAGTGAAAAT AAACTTCGGG ACCTTCAGCA GAAGCAGAG ACTTACAGAA
2051  CTAGAATTCT TGAATTGGAA AGTTCTTTGG AAAAAAGCTT ACAAGAAAC
2101  AAAAATCAGT CAAAAGATTT GGCTGTTCAT CTGGAAGCTG AAAAAAATAA
2151  GCACAATAAG GAGATTACAG TCATGGTTGA AAAACACAAG ACAGAATTGG
2201  AAAGCCTTAA GCATCAGCAG GATGCCCTTT GGACTGAAAA ACTCCAAGTC
2251  TTAAAGCAAC AATATCAGAC TGAAATGGAA AAACTTAGGG AAAAGTGTGA
2301  ACAAGAAAAA GAAACATTGT TGAAAGACAA AGAGATTATC TTCCAGGCCC
2351  ACATAGAAGA AATGAATGAA AAGACTTTAG AAAAGCTTGA TGTGAAGCAA
2401  ACAGAACTAG AATCATTATC TTCTGAACTG TCAGAAGTAT TAAAAGCCCG
2451  TCACAAACTA GAAGAGGAAC TTTCTGTTCT GAAAGATCAA ACAGATAAAA
2501  TGAAGCAGGA ATTAGAGGCC AAGATGGATG AACAGAAAAA TCATCACCAG
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2551    CAGCAAGTTG  ACAGTATCAT  TAAAGAACAC  GAGGTATCTA  TCCAGAGGAC
2601    TGAGAAGGCA  TTAAAAGATC  AAATTAATCA  ACTTGAGCTT  CTCTTGAAGG
2651    AAAGGGACAA  GCATTTGAAA  GAGCATCAGG  CTCATGTAGA  AAATTTAGAG
2701    GCAGATATTA  AAAGGTCTGA  AGGGGAACTC  CAGCAGGCAT  CTGCTAAGCT
2751    GGACGTTTTT  CAGTCTTACC  AGAGTGCCAC  ACATGAGCAG  ACAAAAGCAT
2801    ATGAGGAACA  GTTGGCCCAA  TTGCAGCAGA  AGTTGTTGGA  TTTGGAAACA
2851    GAAAGAATTC  TTCTTACCAA  ACAGGTTGCT  GAAGTTGAAG  CACAAAAGAA
2901    AGATGTTTGT  ACTGAGTTAG  ATGCTCACAA  AATCCAGGTG  CAGGACTTAA
2951    TGCAGCAACT  TGAAAAACAA  AATAGTGAAA  TGGAGCAAAA  AGTAAAATCT
3001    TTAACCCAAG  TCTATGAGTC  CAAACTTGAA  GATGGTAACA  AAGAACAGGA
3051    ACAGACAAAG  CAAATCTTGG  TGGAAAAGGA  AAATATGATT  TTACAAATGA
3101    GAGAAGGACA  GAAGAAAGAA  ATTGAGATAC  TCACACAGAA  ATTGTCAGCC
3151    AAGGAGGACA  GTATTCATAT  TTTGAATGAG  GAATATGAAA  CCAAATTTAA
3201    AAACCAAGAA  AAAAGATGG   AAAAAGTTAA  GCAGAAAGCA  AAGGAGATGC
3251    AAGAAACGTT  AAAGAAAAAA  TTACTGGATC  AGGAAGCCAA  ACTTAAGAAA
3301    GAGCTTGAAA  ATACTGCTCT  AGAGCTTAGT  CAGAAAGAAA  AACAGTTTAA
3351    TGCCAAAATG  CTGGAAATGG  CACAGGCTAA  CTCAGCTGGA  ATCAGTGATG
3401    CAGTGTCAAG  ACTGGAAACA  AACCAAAAAG  AACAAATAGA  AAGTCTTACT
3451    GAGGTTCATC  GACGAGAACT  CAATGATGTC  ATATCAATCT  GGGAAAAGAA
3501    ACTTAATCAG  CAAGCTGAAG  AACTTCAGGA  AATACATGAA  ATCCAATTAC
3551    AGGAAAAAGA  ACAAGAGGTA  GCAGAACTGA  AACAAAGAT   CCTCCTATTT
3601    GGGTGTGAAA  AGAAGAGAT   GAACAAGGAA  ATAACATGGC  TGAAGGAAGA
3651    AGGTGTTAAG  CAGGATACAA  CATTAAATGA  ATTACAGGAA  CAGTTAAAGC
3701    AGAAGTCTGC  CCATGTGAAT  TCTCTTGCAC  AAGATGAAAC  TAAACTGAAA
3751    GCTCATCTTG  AAAAGCTAGA  GGTTGACTTG  AATAAGTCTC  TGAAGGAAAA
3801    TACTTTTCTT  CAAGAGCAGC  TAGTTGAACT  GAAGATGCTG  GCAGAAGAAG
3851    ATAAGCGGAA  GGTTTCTGAG  TTGACTAGCA  AGTTGAAAAC  CACAGATGAA
3901    GAATTCCAGA  GTTTGAAATC  TTCACATGAA  AAAAGTAACA  AAAGCCTAGA
3951    GGACAAGAGC  TTGGAATTTA  AAAAACTGTC  TGAGGAACTA  GCGATTCAGC
4001    TAGATATTTG  CTGTAAGAAA  ACCGAAGCCT  TATTAGAAGC  TAAAACAAAT
4051    GAGCTAATCA  ACATTAGTAG  TAGTAAAACT  AATGCCATTC  TTTCTAGGAT
4101    TTCTCATTGT  CAGCACCGTA  CAACTAAAGT  TAAGGAGGCA  CTGTTAATTA
4151    AAACTTGCAC  AGTTTCTGAA  TTAGAAGCAC  AACTTAGACA  GTTGACAGAG
4201    GAGCAAAATA  CACTAAATAT  TTCTTTTCAA  CAGGCTACTC  ATCAGTTAGA
4251    AGAAAAAGAA  AATCAAATTA  AGAGCATGAA  GGCTGATATT  GAAAGTCTTG
4301    TAACAGAAAA  AGAAGCCTTA  CAGAAGGAAG  GAGGCAATCA  GCAACAGGCT
4351    GCTTCTGAAA  AGGAGTCTTG  TATAACACAG  TTGAAGAAAG  AGTTATCTGA
4401    AAACATCAAT  GCTGTCACAT  TGATGAAAGA  AGAGCTTAAA  GAAAAAAAAG
4451    TTGAGATTAG  CAGTCTTAGT  AAACAACTAA  CTGATTTGAA  TGTTCAGCTT
4501    CAAAATAGCA  TCAGCCTATC  CGAAAAAGAA  GCAGCCATTT  CATCACTAAG
4551    AAAGCAGTAT  GATGAAGAAA  AATGTGAATT  GCTGGATCAG  GTGCAAGATT
4601    TATCTTTTAA  AGTTGACACT  CTGAGTAAAG  AGAAAATTTC  TGCTCTTGAG
4651    CAGGTAGATG  ACTGGTCCAA  TAAATTCTCA  GAATGGAAGA  AGAAAGCACA
4701    GTCAAGATTT  ACACAGCATC  AAAACACTGT  TAAAGAATTG  CAGATCCAGC
4751    TTGAGTTAAA  ATCAAAGGAA  GCTTATGAAA  AGGATGAGCA  GATAAATTTA
4801    TTGAAGGAAG  AGCTTGATCA  GCAAAATAAA  AGATTTGATT  GTTTAAAGGG
4851    TGAAATGGAA  GACGACAAGA  GCAAGATGGA  GAAAAAGGAG  TCTAATTTAG
4901    AAACAGAGTT  AAAGTCTCAA  ACAGCAAGAA  TTATGGAATT  AGAGGACCAT
4951    ATTACCCAGA  AAACTATTGA  AATAGAGTCC  TTAAATGAAG  TTCTTAAAAA
5001    TTACAATCAA  CAAAAGGATA  TTGAACACAA  AGAATTGGTT  CAGAAACTTC
5051    AACATTTTCA  AGAGTTAGGA  GAAGAAAAGG  ACAACAGGGT  TAAAGAAGCT
5101    GAAGAAAAAA  TCTTAACACT  TGAAAACCAA  GTTTATTCCA  TGAAAGCTGA
5151    ACTTGAAACT  AAGAAGAAAG  AATTAGAACA  TGTGAATTTA  AGTGTGAAAA
5201    GCAAAGAGGA  GGAGTTAAAG  GCATTGGAAG  ATAGGCTTGA  GTCAGAAAGT
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5251  GCTGCAAAAT TAGCAGAGTT GAAGAGAAAA GCTGAACAAA AAATTGCTGC
5301  CATTAAGAAG CAGTTGTTAT CTCAAATGGA AGAGAAAGAA GAACAGTATA
5351  AAAAAGGTAC AGAAAGCCAT TTGAGTGAGC TAAATACAAA ATTGCAGGAA
5401  AGAGAAAGGG AAGTTCACAT CTTGGAAGAA AAACTTAAGT CAGTGGAAAG
5451  TTCACAGTCA GAAACATTAA TTGTACCCAG ATCAGCAAAA AATGTGGCAG
5501  CATATACTGA ACAAGAAGAA GCAGATTCCC AAGGCTGTGT GCAGAAGACA
5551  TATGAAGAAA AAATCAGTGT TTTACAAAGA AACTTAACTG AAAAAGAAAA
5601  GCTATTGCAG AGGGTAGGGC AGGAAAAAGA AGAGACAGTT TCTTCTCATT
5651  TTGAAATGCG ATGCCAATAC CAGGAGCGCT TAATAAAGCT AGAACATGCT
5701  GAGGCAAAGC AACATGAAGA TCAAAGTATG ATAGGTCATC TTCAAGAGGA
5751  GCTTGAAGAA AAAAACAAGA AATATTCCTT GATAGTAGCC CAGCATGTGG
5801  AAAAAGAAGG AGGTAAAAAT AACATACAGG CAAAGCAAAA CTTGGAAAAT
5851  GTGTTTGACG ACGTCCAGAA AACCCTCCAG GAGAAGGAAC TAACCTGTCA
5901  GATTTTGGAG CAAAAGATAA AAGAGCTGGA TTCCTGCTTA GTAAGACAGA
5951  AAGAAGTACA TAGAGTTGAA ATGGAAGAGT TGACCTCAAA ATATGAAAAA
6001  TTACAGGCTT TACAACAGAT GGATGGAAGA AATAAACCCA CAGAACTTTT
6051  GGAAGAAAAC ACTGAAGAAA AGTCCAAATC ACATTTGGTC CAACCCAAAT
6101  TGCTTAGTAA CATGGAAGCC CAGCACAATG ATCTGGAGTT TAAATTAGCC
6151  GGGGCAGAAC GGGAGAAACA GAAACTGGGC AAGGAGATTG TTAGATTGCA
6201  GAAAGACCTT CGAATGTTGA GAAAGGAGCA TCAGCAAGAA TTGGAAATAC
6251  TAAAGAAAGA ATATGATCAA GAAAGGGAAG AGAAAATCAA ACAGGAGCAG
6301  GAAGATCTTG AACTGAAGCA CAATTCCACA TTAAAACAGC TGATGAGGGA
6351  GTTTAATACA CAGCTGGCAC AAAAGGAACA AGAGCTGGAA ATGACCATAA
6401  AAGAAACTAT CAATAAGGCC CAGGAGGTGG AGGCTGAACT TTTAGAAAGC
6451  CATCAAGAAG AGACAAATCA GTTACTTAAA AAAATTGCTG AGAAAGATGA
6501  TGATCTAAAA CGAACAGCCA AAGATATGA AGAAATCCTT GATGCTCGTG
6551  AAGAAGAAAT GACTGCAAAA GTAAGGGACC TGCAGACTCA ACTTGAGGAG
6601  CTGCAGAAGA AATACCAGCA AAAGCTAGAG CAGGAGGAGA ACCCTGGCAA
6651  TGATAATGTA ACAATTATGG AGCTACAGAC ACAGCTAGCA CAGAAGACGA
6701  CTTTAATCAG TGATTCGAAA TTGAAAGAGC AAGAGTTCAG AGAACAGATT
6751  CACAATTTAG AAGACCGTTT GAAGAAATAT GAAAAGAATG TATATGCAAC
6801  AACTGTGGGG ACACCTTACA AAGGTGGCAA TTTGTACCAT ACGGATGTCT
6851  CACTCTTTGG AGAACCTACC GAATTTGAGT ATTTGCGAAA AGTGCTTTTT
6901  GAGTATATGA TGGGTCGTGA GACTAAGACC ATGGCAAAAG TTATAACCAC
6951  CGTACTGAAG TTCCCTGATG ATCAGACTCA GAAAATTTTG GAAAGAGAAG
7001  ATGCTCGGCT GATGTTTACT TCACCTCGCA GTGGTATCTT CTGAGTAAAC
7051  CATCAGTCTG TGCTTAGTTA ACATGTGTCA TGGCTCCGAT CTTCATCTTG
7101  AAGAAGAGTG ACATTGGGTG ACTGCTGCTT GGAAAACTGT CCACACTTGC
7151  TACTCTTTGA GAATGAAGTT GTCATTCAGG GCCCCTCATG TAGCCAAAAG
7201  ACCAAGAAAA ATCTGGCCCA CAGATAAGTT GCAGACTGCC TTTAAAATAG
7251  ATTTTATCAG TGGAGAAATG GTGATAGTTT TTTCTTCAGT TTTCTCTTGG
7301  GAAGAGTTTT ATGTTGTTTA AAAGATATTT TGATAACTTA ACCTGCTTTA
7351  TGGGCTTACA TAATATTCCT TTCATCCATT CTTTTTAAAG AACGGCTTAC
7401  CTTTCCTATT TATTTTTAGG GTGATTTTTT AAAAAGACTT GTGCAATACA
7451  TTTTGAGGTG AAACTTAGTG GATTTTTTCT GATAAATTAG AGCATTTAAT
7501  TGACTATTTT ATTCAGGTTG ATCTGTTGAA TATTTGCTAA AGACCAGTTC
7551  TTTAAGCTAA GACATGTAAA AAATCCCAAA TGGCAGTACC TCATTGTTTA
7601  CTTAGCTTTT GTACTTATAT TTTTCAGAGG AAAAAACACT ACTGTAAATT
7651  GTGAATAGCC AATACATAAC TGTATTGTAT GCAAATCTGT GATTGTTGGC
7701  AGTGTCATCT CTGAGAAACA GATAAATAAA GTTTATTTAC TAT
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Fig. 11: SEQ ID NO. 8: amino acid sequence of human golgin-245, splice variant 4

Length: 2252 aa

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   1  MFKKLKQKIS  EEQQQLQQAL  APAQASSNSS  TPTRMRSRTS  SFTEQLDEGT
  51  PNRENASTHA  SKSPDSVNGS  EPSIPQSGDT  QSFAQKLQLR  VPSVESLFRS
 101  PIKESLFRSS  SKESLVRTSS  RESLNRLDLD  SSTASFDPPS  DMDSEAEDLV
 151  GNSDSLNKEQ  LIQRLRRMER  SLSSYRGKYS  ELVTAYQMLQ  REKKKLQGIL
 201  SQSQDKSLRR  IAELREELQM  DQQAKKHLQE  EFDASLEEKD  QYISVLQTQV
 251  SLLKQRLRNG  PMNVDVLKPL  PQLEPQAEVF  TKEENPESDG  EPVVEDGTSV
 301  KTLETLQQRV  KRQENLLKRC  KETIQSHKEQ  CTLLTSEKEA  LQEQLDERLQ
 351  ELEKIKDLHM  AEKTKLITQL  RDAKNLIEQL  EQDKGMVIAE  TKRQMHETLE
 401  MKEEEIAQLR  SRIKQMTTQG  EELREQKEKS  ERAAFEELEK  ALSTAQKTEE
 451  ARRKLKAEMD  EQIKTIEKTS  EEERISLQQE  LSRVKQEVVD  VMKKSSEEQI
 501  AKLQKLHEKE  LARKEQELTK  KLQTREREFQ  EQMKVALEKS  QSEYLKISQE
 551  KEQQESLALE  ELELQKKAIL  TESENKLRDL  QQEAETYRTR  ILELESSLEK
 601  SLQENKNQSK  DLAVHLEAEK  NKHNKEITVM  VEKHKTELES  LKHQQDALWT
 651  EKLQVLKQQY  QTEMEKLREK  CEQEKETLLK  DKEIIFQAHI  EEMNEKTLEK
 701  LDVKQTELES  LSSELSEVLK  ARHKLEEELS  VLKDQTDKMK  QELEAKMDEQ
 751  KNHHQQQVDS  IIKEHEVSIQ  RTEKALKDQI  NQLELLLKER  DKHLKEHQAH
 801  VENLEADIKR  SEGELQQASA  KLDVFQSYQS  ATHEQTKAYE  EQLAQLQQKL
 851  LDLETERILL  TKQVAEVEAQ  KKDVCTELDA  HKIQVQDLMQ  QLEKQNSEME
 901  QKVKSLTQVY  ESKLEDGNKE  QEQTKQILVE  KENMILQMRE  GQKKEIEILT
 951  QKLSAKEDSI  HILNEEYETK  FKNQEKKMEK  VKQKAKEMQE  TLKKKLLDQE
1001  AKLKKELENT  ALELSQKEKQ  FNAKMLEMAQ  ANSAGISDAV  SRLETNQKEQ
1051  IESLTEVHRR  ELNDVISIWE  KKLNQQAEEL  QEIHEIQLQE  KEQEVAELKQ
1101  KILLFGCEKE  EMNKEITWLK  EEGVKQDTTL  NELQEQLKQK  SAHVNSLAQD
1151  ETKLKAHLEK  LEVDLNKSLK  ENTFLQEQLV  ELKMLAEEDK  RKVSELTSKL
1201  KTTDEEFQSL  KSSHEKSNKS  LEDKSLEFKK  LSEELAIQLD  ICCKKTEALL
1251  EAKTNELINI  SSSKTNAILS  RISHCQHRTT  KVKEALLIKT  CTVSELEAQL
1301  RQLTEEQNTL  NISFQQATHQ  LEEKENQIKS  MKADIESLVT  EKEALQKEGG
1351  NQQQAASEKE  SCITQLKKEL  SENINAVTLM  KEELKEKKVE  ISSLSKQLTD
1401  LNVQLQNSIS  LSEKEAAISS  LRKQYDEEKC  ELLDQVQDLS  FKVDTLSKEK
1451  ISALEQVDDW  SNKFSEWKKK  AQSRFTQHQN  TVKELQIQLE  LKSKEAYEKD
1501  EQINLLKEEL  DQQNKRFDCL  KGEMEDDKSK  MEKKESNLET  ELKSQTARIM
1551  ELEDHITQKT  IEIESLNEVL  KNYNQQKDIE  HKELVQKLQH  FQELGEEKDN
1601  RVKEAEEKIL  TLENQVYSMK  AELETKKKEL  EHVNLSVKSK  EEELKALEDR
1651  LESESAAKLA  ELKRKAEQKI  AAIKKQLLSQ  MEEKEEQYKK  GTESHLSELN
1701  TKLQEREREV  HILEEKLKSV  ESSQSETLIV  PRSAKNVAAY  TEQEEADSQG
1751  CVQKTYEEKI  SVLQRNLTEK  EKLLQRVGQE  KEETVSSHFE  MRCQYQERLI
1801  KLEHAEAKQH  EDQSMIGHLQ  EELEEKNKKY  SLIVAQHVEK  EGGKNNIQAK
1851  QNLENVFDDV  QKTLQEKELT  CQILEQKIKE  LDSCLVRQKE  VHRVEMEELT
1901  SKYEKLQALQ  QMDGRNKPTE  LLEENTEEKS  KSHLVQPKLL  SNMEAQHNDL
1951  EFKLAGAERE  KQKLGKEIVR  LQKDLRMLRK  EHQQELEILK  KEYDQEREEK
2001  IKQEQEDLEL  KHNSTLKQLM  REFNTQLAQK  EQELEMTIKE  TINKAQEVEA
2051  ELLESHQEET  NQLLKKIAEK  DDDLKRTAKR  YEEILDAREE  EMTAKVRDLQ
2101  TQLEELQKKY  QQKLEQEENP  GNDNVTIMEL  QTQLAQKTTL  ISDSKLKEQE
2151  FREQIHNLED  RLKKYEKNVY  ATTVGTPYKG  GNLYHTDVSL  FGEPTEFEYL
2201  RKVLFEYMMG  RETKTMAKVI  TTVLKFPDDQ  TQKILEREDA  RLMFTSPRSG
2251  IF
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-18/25-

Fig. 12: SEQ ID NO. 9: nucleotide sequence of human golgin-245 cDNA, splice variant 4

Length: 7761 bp

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   1   GCAACGAAGG  TACCATGGCC  GTTGTCGTCG  CCGCCGCGGC  TCCCGGGGCT
  51   GGATGGGGGG  CCGAGGCCAG  CCAGTGGCAC  CCGGAAGAAA  GAGACGCGGC
 101   GGCGGCGACG  CCGACACCCT  CAGGACGAGT  GTCCGGACTT  GCCCACAGCC
 151   TCAAGGAGGA  GACGGCGAGG  CCCGGCCCCC  GCTGTCCCTG  GTGTAAAGAA
 201   GTCGCCGTAG  CCGTCGCGGC  CGGGACTCCC  CGGGCTCTCG  CCCTTCAGGT
 251   TTCGTTGACA  CTCAGGACCG  TACGTACGCT  GCGCCATGTT  CAAGAAACTG
 301   AAGCAAAAGA  TCAGCGAGGA  GCAGCAGCAG  CTCCAGCAGG  CGCTGGCTCC
 351   TGCTCAGGCG  TCCTCCAATT  CTTCAACACC  AACAAGAATG  AGGAGCAGGA
 401   CATCTTCATT  TACAGAGCAA  CTTGATGAAG  GTACACCCAA  TAGAGAGAAT
 451   GCATCTACTC  ATGCCTCGAA  ATCTCCTGAC  AGTGTTAATG  GAAGTGAACC
 501   AAGCATTCCT  CAGTCAGGTG  ACACACAGTC  TTTTGCACAG  AAGCTCCAGC
 551   TCCGGGTGCC  CTCCGTGGAG  TCTTTGTTTC  GAAGTCCGAT  AAAGGAATCT
 601   CTATTCCGGT  CTTCTTCTAA  AGAGTCTTTG  GTACGAACAT  CTTCCAGAGA
 651   ATCCCTGAAT  CGACTTGACC  TGGACAGTTC  TACTGCCAGT  TTTGATCCAC
 701   CCTCTGATAT  GGATAGCGAG  GCTGAAGACT  TGGTAGGGAA  TTCAGACAGT
 751   CTCAACAAAG  AACAGTTGAT  TCAGCGGTTG  CGAAGAATGG  AACGAAGCTT
 801   AAGTAGCTAC  AGGGGAAAAT  ATTCTGAGCT  TGTTACAGCT  TATCAGATGC
 851   TTCAGAGAGA  GAAGAAAAAG  CTACAAGGTA  TATTAAGTCA  GAGTCAGGAT
 901   AAATCACTTC  GGAGAATAGC  AGAATTAAGA  GAGGAGCTCC  AAATGGACCA
 951   GCAGGCAAAG  AAACATCTGC  AAGAGGAGTT  TGATGCATCT  TTAGAGGAGA
1001   AAGATCAGTA  TATCAGTGTT  CTCCAAACTC  AGGTTTCTCT  ACTGAAACAA
1051   CGATTACGAA  ATGGCCCGAT  GAATGTTGAT  GTACTGAAAC  CACTTCCTCA
1101   GCTGGAACCA  CAGGCTGAAG  TCTTCACTAA  AGAAGAGAAT  CCAGAAAGTG
1151   ATGGAGAGCC  AGTAGTGGAA  GATGGAACTT  CTGTAAAAAC  ACTGGAAACA
1201   CTCCAGCAAA  GAGTGAAGCG  TCAAGAGAAC  CTACTTAAGC  GTTGTAAGGA
1251   AACAATTCAG  TCACATAAGG  AACAATGTAC  ACTATTAACT  AGTGAAAAAG
1301   AAGCTCTGCA  AGAACAACTG  GATGAAAGAC  TTCAAGAACT  AGAAAAGATA
1351   AAGGACCTTC  ATATGGCCGA  GAAGACTAAA  CTTATCACTC  AGTTGCGTGA
1401   TGCAAAGAAC  TTAATTGAAC  AGCTTGAACA  AGATAAGGGA  ATGGTAATCG
1451   CAGAGACAAA  ACGTCAGATG  CATGAAACCC  TGGAAATGAA  AGAAGAAGAA
1501   ATTGCTCAAC  TCCGTAGTCG  CATCAAACAG  ATGACTACCC  AGGGAGAGGA
1551   ATTACGGGAA  CAGAAAGAAA  AGTCCGAAAG  AGCTGCTTTT  GAGGAACTTG
1601   AAAAAGCTTT  GAGTACAGCC  CAAAAAACAG  AGGAAGCACG  GAGAAAACTG
1651   AAGGCAGAAA  TGGATGAACA  AATAAAAACT  ATCGAAAAAA  CAAGTGAGGA
1701   GGAACGCATC  AGTCTTCAAC  AGGAATTAAG  TCGGGTGAAA  CAGGAGGTTG
1751   TTGATGTAAT  GAAAAAATCC  TCAGAAGAAC  AAATTGCTAA  GCTACAGAAG
1801   CTTCATGAAA  AGGAGCTGGC  CAGAAAGAG   CAGGAACTGA  CCAAGAAGCT
1851   TCAGACCCGA  GAAAGGGAAT  TTCAGGAACA  AATGAAAGTA  GCTCTTGAAA
1901   AGAGTCAATC  AGAATATTTG  AAGATCAGCC  AAGAAAAAGA  ACAGCAAGAA
1951   TCTTTGGCCC  TAGAAGAGTT  AGAGTTGCAG  AAAAAAGCAA  TCCTCACAGA
2001   AAGTGAAAAT  AAACTTCGGG  ACCTTCAGCA  AGAAGCAGAG  ACTTACAGAA
2051   CTAGAATTCT  TGAATTGGAA  AGTTCTTTGG  AAAAAAGCTT  ACAAGAAAC
2101   AAAAATCAGT  CAAAGATTT   GGCTGTTCAT  CTGGAAGCTG  AAAAAAATAA
2151   GCACAATAAG  GAGATTACAG  TCATGGTTGA  AAAACACAAG  ACAGAATTGG
2201   AAAGCCTTAA  GCATCAGCAG  GATGCCCTTT  GGACTGAAAA  ACTCCAAGTC
2251   TTAAAGCAAC  AATATCAGAC  TGAAATGGAA  AAACTTAGGG  AAAAGTGTGA
2301   ACAAGAAAAA  GAAACATTGT  TGAAAGACAA  AGAGATTATC  TTCCAGGCCC
2351   ACATAGAAGA  AATGAATGAA  AAGACTTTAG  AAAAGCTTGA  TGTGAAGCAA
2401   ACAGAACTAG  AATCATTATC  TTCTGAACTG  TCAGAAGTAT  TAAAAGCCCG
2451   TCACAAACTA  GAAGAGGAAC  TTTCTGTTCT  GAAAGATCAA  ACAGATAAAA
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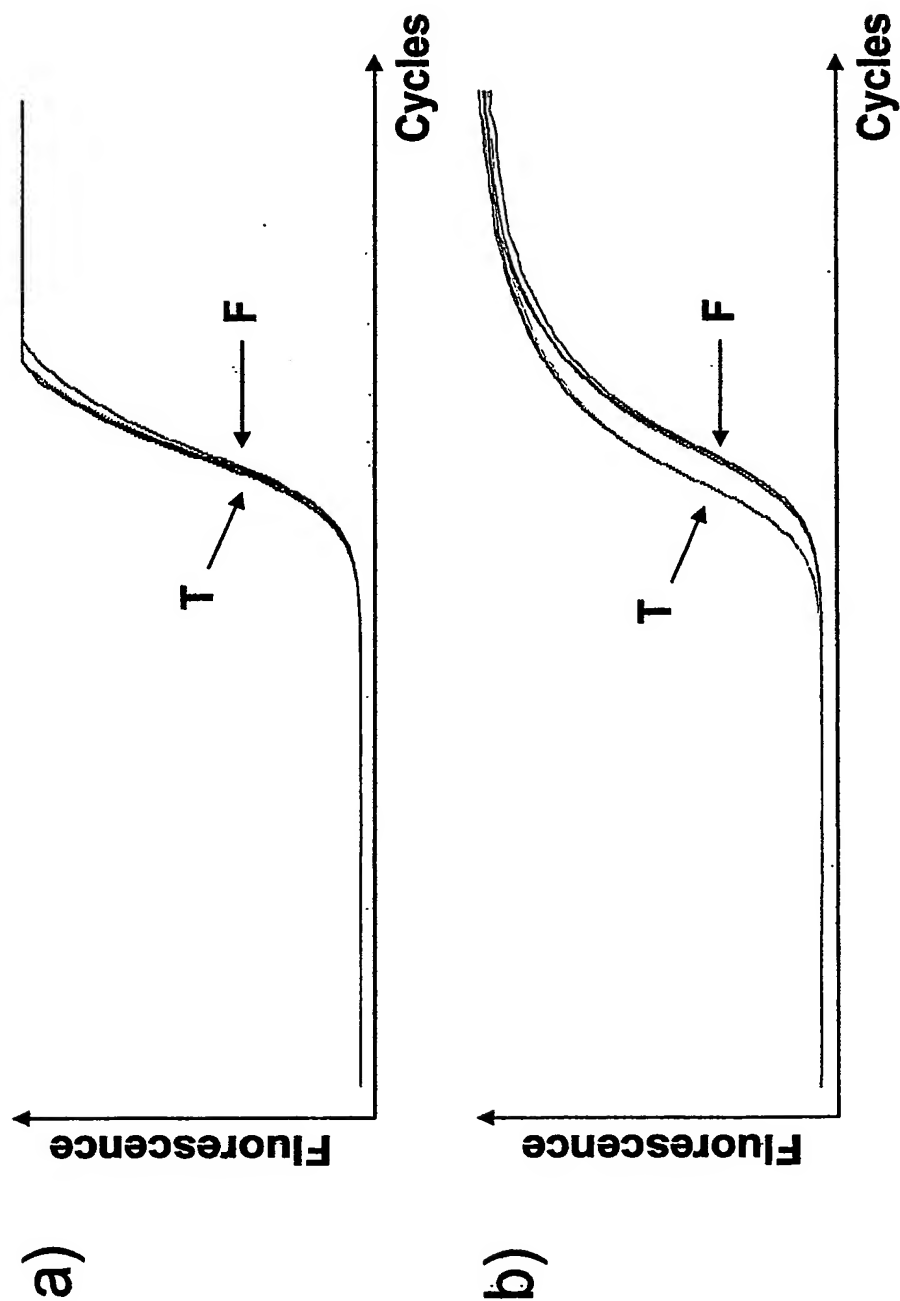
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2551  CAGCAAGTTG ACAGTATCAT TAAAGAACAC GAGGTATCTA TCCAGAGGAC
2601  TGAGAAGGCA TTAAAAGATC AAATTAATCA ACTTGAGCTT CTCTTGAAGG
2651  AAAGGGACAA GCATTTGAAA GAGCATCAGG CTCATGTAGA AAATTTAGAG
2701  GCAGATATTA AAAGGTCTGA AGGGGAACTC CAGCAGGCAT CTGCTAAGCT
2751  GGACGTTTTT CAGTCTTACC AGAGTGCCAC ACATGAGCAG ACAAAAGCAT
2801  ATGAGGAACA GTTGGCCCAA TTGCAGCAGA AGTTGTTGGA TTTGGAAACA
2851  GAAAGAATTC TTCTTACCAA ACAGGTTGCT GAAGTTGAAG CACAAAAGAA
2901  AGATGTTTGT ACTGAGTTAG ATGCTCACAA AATCCAGGTG CAGGACTTAA
2951  TGCAGCAACT TGAAAAACAA AATAGTGAAA TGGAGCAAAA AGTAAAATCT
3001  TTAACCCAAG TCTATGAGTC CAAACTTGAA GATGGTAACA AAGAACAGGA
3051  ACAGACAAAG CAAATCTTGG TGGAAAAGGA AAATATGATT TTACAAATGA
3101  GAGAAGGACA GAAGAAAGAA ATTGAGATAC TCACACAGAA ATTGTCAGCC
3151  AAGGAGGACA GTATTCATAT TTTGAATGAG GAATATGAAA CCAAATTTAA
3201  AAACCAAGAA AAAAGATGG AAAAAGTTAA GCAGAAAGCA AAGGAGATGC
3251  AAGAAACGTT AAAGAAAAAA TTACTGGATC AGGAAGCCAA ACTTAAGAAA
3301  GAGCTTGAAA ATACTGCTCT AGAGCTTAGT CAGAAAGAAA AACAGTTTAA
3351  TGCCAAAATG CTGGAAATGG CACAGGCTAA CTCAGCTGGA ATCAGTGATG
3401  CAGTGTCAAG ACTGGAAACA AACCAAAAAG AACAAATAGA AAGTCTTACT
3451  GAGGTTCATC GACGAGAACT CAATGATGTC ATATCAATCT GGGAAAAGAA
3501  ACTTAATCAG CAAGCTGAAG AACTTCAGGA AATACATGAA ATCCAATTAC
3551  AGGAAAAAGA ACAAGAGGTA GCAGAACTGA AACAAAGAT CCTCCTATTT
3601  GGGTGTGAAA AAGAAGAGAT GAACAAGGAA ATAACATGGC TGAAGGAAGA
3651  AGGTGTTAAG CAGGATACAA CATTAAATGA ATTACAGGAA CAGTTAAAGC
3701  AGAAGTCTGC CCATGTGAAT TCTCTTGCAC AAGATGAAAC TAAACTGAAA
3751  GCTCATCTTG AAAAGCTAGA GGTTGACTTG AATAAGTCTC TGAAGGAAAA
3801  TACTTTTCTT CAAGAGCAGC TAGTTGAACT GAAGATGCTG GCAGAAGAAG
3851  ATAAGCGGAA GGTTTCTGAG TTGACTAGCA AGTTGAAAAC CACAGATGAA
3901  GAATTCCAGA GTTTGAAATC TTCACATGAA AAAAGTAACA AAAGCCTAGA
3951  GGACAAGAGC TTGGAATTTA AAAAACTGTC TGAGGAACTA GCGATTCAGC
4001  TAGATATTTG CTGTAAGAAA ACCGAAGCCT TATTAGAAGC TAAAACAAAT
4051  GAGCTAATCA ACATTAGTAG TAGTAAAACT AATGCCATTC TTTCTAGGAT
4101  TTCTCATTGT CAGCACCGTA CAACTAAAGT TAAGGAGGCA CTGTTAATTA
4151  AAACTTGCAC AGTTTCTGAA TTAGAAGCAC AACTTAGACA GTTGACAGAG
4201  GAGCAAAATA CACTAAATAT TTCTTTTCAA CAGGCTACTC ATCAGTTAGA
4251  AGAAAAAGAA AATCAAATTA AGAGCATGAA GGCTGATATT GAAAGTCTTG
4301  TAACAGAAAA AGAAGCCTTA CAGAAGGAAG GAGGCAATCA GCAACAGGCT
4351  GCTTCTGAAA AGGAGTCTTG TATAACACAG TTGAAGAAAG AGTTATCTGA
4401  AAACATCAAT GCTGTCACAT TGATGAAAGA AGAGCTTAAA GAAAAAAAAG
4451  TTGAGATTAG CAGTCTTAGT AAACAACTAA CTGATTTGAA TGTTCAGCTT
4501  CAAAATAGCA TCAGCCTATC CGAAAAAGAA GCAGCCATTT CATCACTAAG
4551  AAAGCAGTAT GATGAAGAAA AATGTGAATT GCTGGATCAG GTGCAAGATT
4601  TATCTTTTAA AGTTGACACT CTGAGTAAAG AGAAAATTTC TGCTCTTGAG
4651  CAGGTAGATG ACTGGTCCAA TAAATTCTCA GAATGGAAGA AGAAAGCACA
4701  GTCAAGATTT ACACAGCATC AAAACACTGT TAAAGAATTG CAGATCCAGC
4751  TTGAGTTAAA ATCAAAGGAA GCTTATGAAA AGGATGAGCA GATAAATTTA
4801  TTGAAGGAAG AGCTTGATCA GCAAAATAAA AGATTTGATT GTTAAAGGG
4851  TGAAATGGAA GACGACAAGA GCAAGATGGA GAAAAAGGAG TCTAATTTAG
4901  AAACAGAGTT AAAGTCTCAA ACAGCAAGAA TTATGGAATT AGAGGACCAT
4951  ATTACCCAGA AAACTATTGA AATAGAGTCC TTAAATGAAG TTCTTAAAAA
5001  TTACAATCAA CAAAAGGATA TTGAACACAA AGAATTGGTT CAGAAACTTC
5051  AACATTTTCA AGAGTTAGGA GAAGAAAAGG ACAACAGGGT TAAAGAAGCT
5101  GAAGAAAAAA TCTTAACACT TGAAAACCAA GTTTATTCCA TGAAAGCTGA
5151  ACTTGAAACT AAGAAGAAAG AATTAGAACA TGTGAATTTA AGTGTGAAAA
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5201   GCAAAGAGGA GGAGTTAAAG GCATTGGAAG ATAGGCTTGA GTCAGAAAGT
5251   GCTGCAAAAT TAGCAGAGTT GAAGAGAAAA GCTGAACAAA AAATTGCTGC
5301   CATTAAGAAG CAGTTGTTAT CTCAAATGGA AGAGAAAGAA GAACAGTATA
5351   AAAAAGGTAC AGAAAGCCAT TTGAGTGAGC TAAATACAAA ATTGCAGGAA
5401   AGAGAAAGGG AAGTTCACAT CTTGGAAGAA AAACTTAAGT CAGTGGAAAG
5451   TTCACAGTCA GAAACATTAA TTGTACCCAG ATCAGCAAAA AATGTGGCAG
5501   CATATACTGA ACAAGAAGAA GCAGATTCCC AAGGCTGTGT GCAGAAGACA
5551   TATGAAGAAA AAATCAGTGT TTTACAAAGA AACTTAACTG AAAAAGAAAA
5601   GCTATTGCAG AGGGTAGGGC AGGAAAAAGA AGAGACAGTT TCTTCTCATT
5651   TTGAAATGCG ATGCCAATAC CAGGAGCGCT TAATAAAGCT AGAACATGCT
5701   GAGGCAAAGC AACATGAAGA TCAAAGTATG ATAGGTCATC TTCAAGAGGA
5751   GCTTGAAGAA AAAAACAAGA AATATTCCTT GATAGTAGCC CAGCATGTGG
5801   AAAAAGAAGG AGGTAAAAAT AACATACAGG CAAAGCAAAA CTTGGAAAAT
5851   GTGTTTGACG ACGTCCAGAA AACCCTCCAG GAGAAGGAAC TAACCTGTCA
5901   GATTTTGGAG CAAAAGATAA AAGAGCTGGA TTCCTGCTTA GTAAGACAGA
5951   AAGAAGTACA TAGAGTTGAA ATGGAAGAGT TGACCTCAAA ATATGAAAAA
6001   TTACAGGCTT TACAACAGAT GGATGGAAGA AATAAACCCA CAGAACTTTT
6051   GGAAGAAAAC ACTGAAGAAA AGTCCAAATC ACATTTGGTC CAACCCAAAT
6101   TGCTTAGTAA CATGGAAGCC CAGCACAATG ATCTGGAGTT TAAATTAGCC
6151   GGGGCAGAAC GGGAGAAACA GAAACTGGGC AAGGAGATTG TTAGATTGCA
6201   GAAAGACCTT CGAATGTTGA GAAAGGAGCA TCAGCAAGAA TTGGAAATAC
6251   TAAAGAAAGA ATATGATCAA GAAAGGGAAG AGAAAATCAA ACAGGAGCAG
6301   GAAGATCTTG AACTGAAGCA CAATTCCACA TTAAAACAGC TGATGAGGGA
6351   GTTTAATACA CAGCTGGCAC AAAAGGAACA AGAGCTGGAA ATGACCATAA
6401   AAGAAACTAT CAATAAGGCC CAGGAGGTGG AGGCTGAACT TTTAGAAAGC
6451   CATCAAGAAG AGACAAATCA GTTACTTAAA AAAATTGCTG AGAAAGATGA
6501   TGATCTAAAA CGAACAGCCA AAGATATGA AGAAATCCTT GATGCTCGTG
6551   AAGAAGAAAT GACTGCAAAA GTAAGGGACC TGCAGACTCA ACTTGAGGAG
6601   CTGCAGAAGA AATACCAGCA AAAGCTAGAG CAGGAGGAGA ACCCTGGCAA
6651   TGATAATGTA ACAATTATGG AGCTACAGAC ACAGCTAGCA CAGAAGACGA
6701   CTTTAATCAG TGATTCGAAA TTGAAAGAGC AAGAGTTCAG AGAACAGATT
6751   CACAATTTAG AAGACCGTTT GAAGAAATAT GAAAGAATG TATATGCAAC
6801   AACTGTGGGG ACACCTTACA AAGGTGGCAA TTTGTACCAT ACGGATGTCT
6851   CACTCTTTGG AGAACCTACC GAATTTGAGT ATTTGCGAAA AGTGCTTTTT
6901   GAGTATATGA TGGGTCGTGA GACTAAGACC ATGGCAAAAG TTATAACCAC
6951   CGTACTGAAG TTCCCTGATG ATCAGACTCA GAAAATTTTG GAAAGAGAAG
7001   ATGCTCGGCT GATGTTTACT TCACCTCGCA GTGGTATCTT CTGAGTAAAC
7051   CATCAGTCTG TGCTTAGTTA ACATGTGTCA TGGCTCCGAT CTTCATCTTG
7101   AAGAAGAGTG ACATTGGGTG ACTGCTGCTT GGAAAACTGT CCACACTTGC
7151   TACTCTTTGA GAATGAAGTT GTCATTCAGG GCCCCTCATG TAGCCAAAAG
7201   ACCAAGAAAA ATCTGGCCCA CAGATAAGTT GCAGACTGCC TTTAAAATAG
7251   ATTTTATCAG TGGAGAAATG GTGATAGTTT TTTCTTCAGT TTTCTCTTGG
7301   GAAGGAGTTT TATGTTGTTT AAAAGATATT TTGATAACTT AACCTGCTTT
7351   ATGGGCTTAC ATAATATTCC TTTCATCCAT TCTTTTTAAA GAACGGCTTA
7401   CCTTTCCTAT TTATTTTTAG GGTGATTTTT TAAAAAGACT TGTGCAATAC
7451   ATTTTGAGGT GAAACTTAGT GGATTTTTTC TGATAAATTA GAGCATTTAA
7501   TTGACTATTT TATTCAGGTT GATCTGTTGA ATATTTGCTA AAGACCAGTT
7551   CTTTAAGCTA AGACATGTAA AAAATCCCAA ATGGCAGTAC CTCATTGTTT
7601   ACTTAGCTTT TGTACTTATA TTTTTCAGAG GAAAAAACAC TACTGTAAAT
7651   TGTGAATAGC CAATACATAA CTGTATTGTA TGCAAATCTG TGATTGTTGG
7701   CAGTGTCATC TCTGAGAAAC AGATAAATAA AGTTTATTTA CTATAAAAAA
7751   AAAAAAAAAA G
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Fig. 13: Verification of differential expression of golgin-245 splice variant 1 and/or 3 by quantitative RT-PCR

a)

b)

Fig. 14: Verification of differential expression of golgin-245 splice variant 1 and/or 3 by quantitative RT-PCR
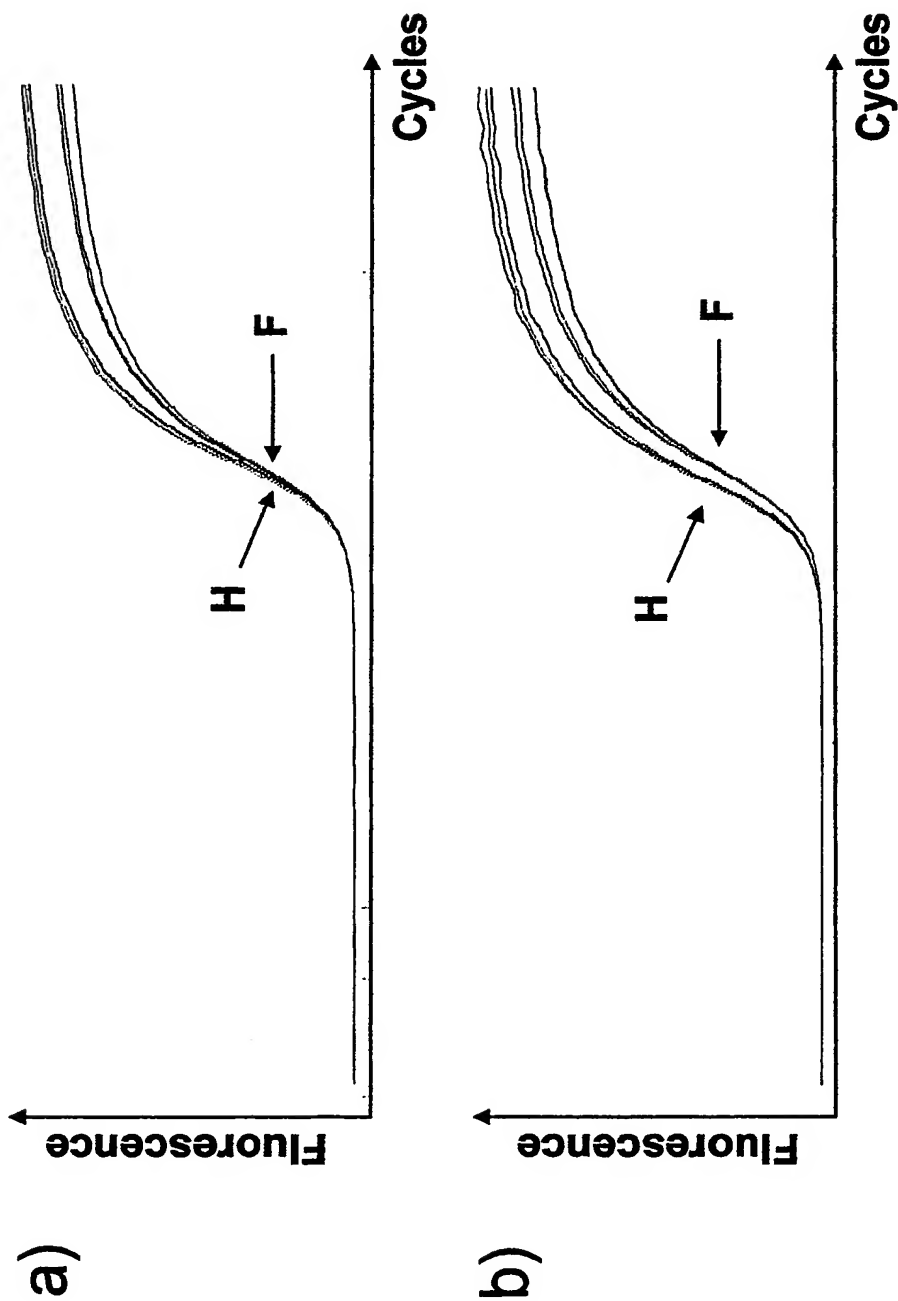
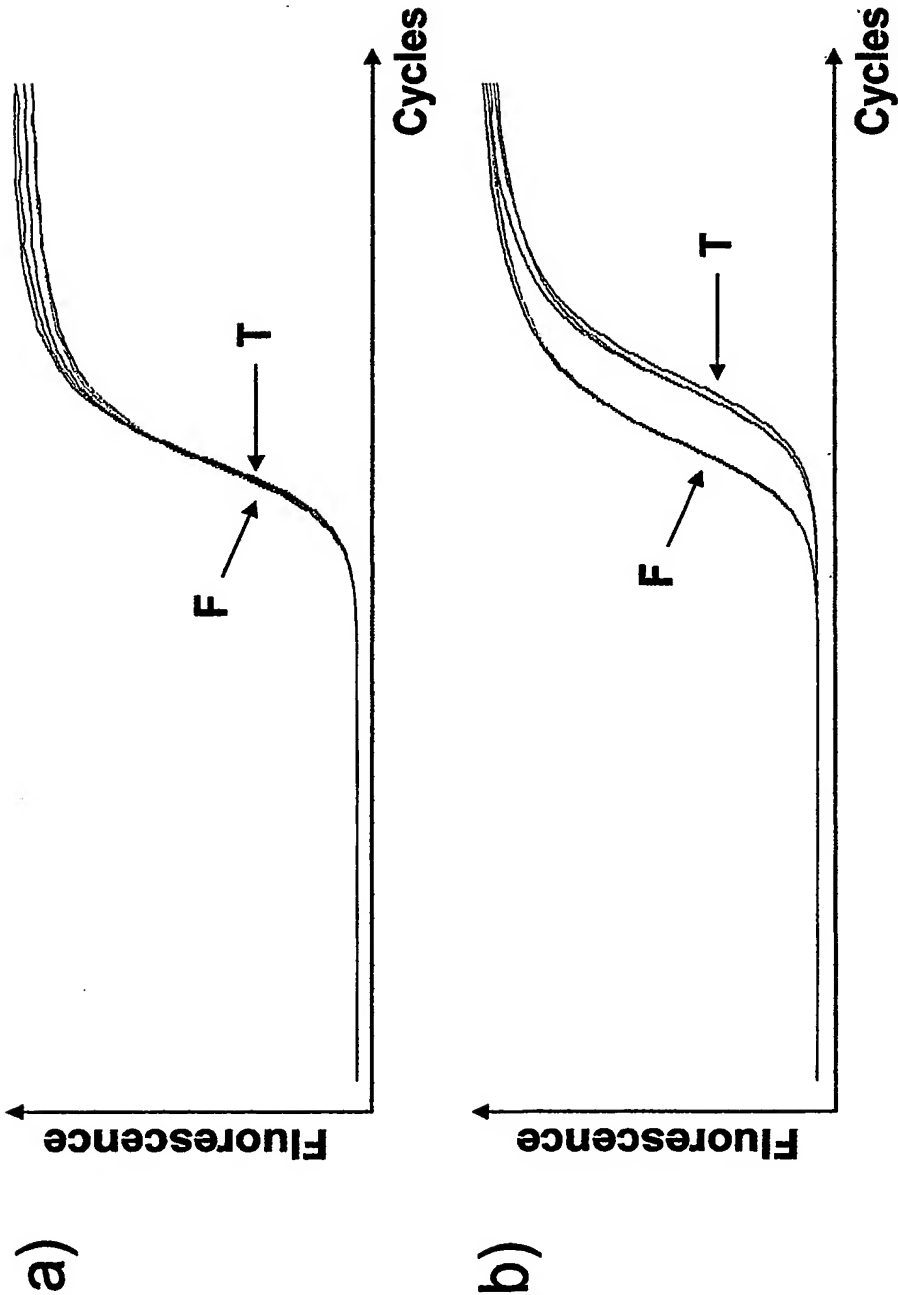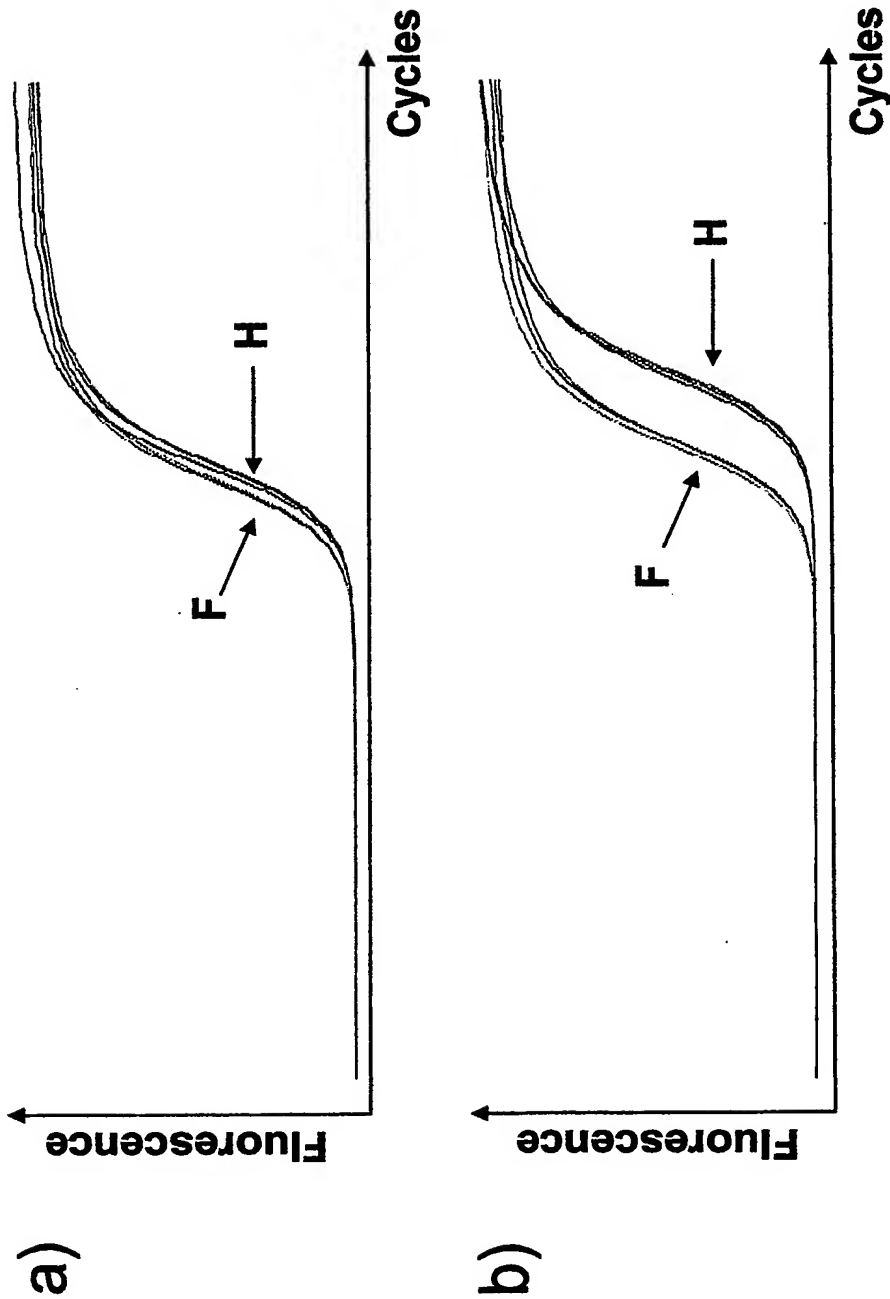Fig. 15: Verification of differential expression of golgin-245 splice variant 2 and/or 4 by quantitative RT-PCR

Fig. 16: Verification of differential expression of golgin-245 splice variant 2 and/or 4 by quantitative RT-PCR

Fig. 17: Images of the human cerebral cortex labeled with anti-golgin-245 monoclonal antibody and with DAPI